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[Continued on next page]

(54) Title: EUKARYOTIC CELL DIVISION GENES AND THEIR USE IN DIAGNOSIS AND TREATMENT OF PROLIFERA-
TIVE DISEASES

Multiple Sequence Alignment of the H38K22.2a family

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CeH38K22.2a  ---MNRLES-DQRTKLRQFVQWRCVTEAVSINFLAKANNINIEVAMTLYEDNINLFGAGSTP
CeH38K22.2b  ---MNRLES-DQ-----
DmCG7427     MILONLSSSTHRDKVKKEISLTHGTOTAFCLQONDKKFSASDNVEONHEYYRYE--
MmAAF04863   ---MNRLES-SQDKVROEMIFTCSSKTAUSCTSONDKLQVATDNFFONPELYIRESV
HsAAH09478   ---MNRLES-SQDKVROEMIFTCSSKTAUSCTSONDKLQVATDNFFONPELYIRESV

CeH38K22.2a  QPSVDSNTEREFNCFYVDEKDKVGEKRMGPHGINRLTDLGYEATDRRLVLAWEETQOT
CeH38K22.2b  ---KTKLEREFNCFYVDEKDKVGEKRMGPHGINRLTDLGYEATDRRLVLAWEETQOT
DmCG7427     ---LTKKRISQIFMRYRDESD---PLKISQSVIHFLEEDLKPDSKLVLLATVSHHEEV
MmAAF04863   KGSQDKKKKQLYTRYVDDOD---ENKISIDSLQOQFCDDALDPASISVLAWEETQOT
HsAAH09478   KGSQDKKKKQLYTRYVDDOD---ENKISIDSLQOQFCDDALDPASISVLAWEETQOT

CeH38K22.2a  QSESLDEWVKMTALQADTVONTRQRTDSINSGLESKAKHELYLEAFNYRASAACRN
CeH38K22.2b  QSESLDEWVKMTALQADTVONTRQRTDSINSGLESKAKHELYLEAFNYRASAACRN
DmCG7427     QSESRDEFINGCDLGIDSDKLTCKPILEQETN-DAGEKDFYHFTNYRQDPQCG
MmAAF04863   QSESRQDFMDGTELGCDSEKIKRQEPKMEQEK-EPGRKDFYHFTNYRQDPQCG
HsAAH09478   QSESRQDFMDGTELGCDSEKIKRQEPKMEQEK-EPGRKDFYHFTNYRQDPQCG

CeH38K22.2a  EDLETATCCNDVLEFGORSTIMTOWIDELWAQENAAASRLAQNVGASNAKQFSVWISRT
CeH38K22.2b  EDLETATCCNDVLEFGORSTIMTOWIDELWAQENAAASRLAQNVGASNAKQFSVWISRT
DmCG7427     EDLETATCCNDVLEFGORSTIMTOWIDELWAQENAAASRLAQNVGASNAKQFSVWISRT
MmAAF04863   EDLETATCCNDVLEFGORSTIMTOWIDELWAQENAAASRLAQNVGASNAKQFSVWISRT
HsAAH09478   EDLETATCCNDVLEFGORSTIMTOWIDELWAQENAAASRLAQNVGASNAKQFSVWISRT

CeH38K22.2a  NTFWDEILLSKFDLSQVDDDEGAWGQVDDQDYCRENLNYPKPGNASNDQOMETPKIAQ
CeH38K22.2b  NTFWDEILLSKFDLSQVDDDEGAWGQVDDQDYCRENLNYPKPGNASNDQOMETPKIAQ
DmCG7427     NTFWDEILLSKFDLSQVDDDEGAWGQVDDQDYCRENLNYPKPGNASNDQOMETPKIAQ
MmAAF04863   NTFWDEILLSKFDLSQVDDDEGAWGQVDDQDYCRENLNYPKPGNASNDQOMETPKIAQ
HsAAH09478   NTFWDEILLSKFDLSQVDDDEGAWGQVDDQDYCRENLNYPKPGNASNDQOMETPKIAQ

CeH38K22.2a  KKPGIFYFNSNLQIEFKLFQYFMLEKTIKTIITAGTNR
CeH38K22.2b  KKPGIFYFNSNLQIEFKLFQYFMLEKTIKTIITAGTNR
DmCG7427     SQKNISSAYQTSHTNMNYG-----
MmAAF04863   -----
HsAAH09478   -----
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(57) Abstract: The present invention relates to the significant functional role of several *C. elegans* genes and of their corresponding gene products in cell division and proliferation processes that could be identified by means of RNA-mediated interference (RNAi) and to the identification and isolation of functional orthologues of said genes including all biologically-active derivatives thereof. The invention further relates to the use of said gene products (including said orthologues) in the development or isolation of anti-proliferative agents, particularly their use in appropriate screening assays, and their use for diagnosis and treatment of proliferative diseases.

Statistics	HsAAH09478	MmAAF04863	DmCG7427
CeH38K22.2a	E-value: 1e-49 Identities: 101/275 (36%) Positives: 158/275 (56%)	E-value: 7e-48 Identities: 100/275 (36%) Positives: 157/275 (56%)	E-value: 6e-44 Identities: 104/299 (36%) Positives: 154/299 (56%)
CeH38K22.2b	E-value: 1e-49 Identities: 101/275 (36%) Positives: 158/275 (56%)	E-value: 7e-48 Identities: 100/275 (36%) Positives: 157/275 (56%)	E-value: 6e-44 Identities: 104/299 (36%) Positives: 154/299 (56%)



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**Eukaryotic cell division genes and their use in diagnosis and treatment of
proliferative diseases**

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In a first aspect, the present invention is related to the significant functional role of several *C. elegans* genes and of their corresponding gene products in cell division and proliferation processes that could be identified by means of RNA-mediated interference (RNAi).

10 In a second aspect, the invention relates to the identification and isolation of functional orthologues of said genes and their gene products found in other eukaryotic species, in particular man, including all biologically-active derivatives thereof.

In a third aspect, the present invention includes the use of said genes and gene products (including said orthologues) in the development or isolation of anti-proliferative agents for instance their use in appropriate screening assays and in methods for diagnosis and
15 treatment of proliferative diseases.

In a forth aspect, the invention relates to antibodies to said gene products and their use in the development or isolation of anti-proliferative agents and in methods for diagnosis and treatment of proliferative diseases.

20 In a fifth aspect, the present invention is related to the use of these genes and gene products for developing structural models or other models for evaluating drug binding and efficacy as well as to any other uses which are derived from the new functions described here and which will become apparent from the disclosure of the present application for any person skilled in the art.

25 Metazoan cell division consists of an extremely complex, highly regulated set of cellular processes which must be tightly co-ordinated, perfectly timed, and closely monitored in order to ensure the correct delivery of cellular materials to daughter cells. Defects in these processes are known to cause a wide range of so-called proliferative diseases, including all forms of cancer. Since cell division represents one of the few, if not the only cellular
30 process that is common to the aetiology of all forms of cancer, its specific inhibition has

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long been recognised as a preferred site of therapeutic intervention. Although mitotic inhibitor drugs are recognised as one of the most promising classes of chemotherapeutic agent, screening attempts to find new drug candidates in this class have been undermined by the strong inherent tendency of such screens to identify agents that target a single
5 protein, tubulin. Tubulin polymerises to form microtubules, the primary cytoskeletal elements needed for mitotic spindle function and chromosome segregation. Microtubule functions, however, are ubiquitously needed in almost all cell types, whether dividing or not, a fact which therefore explains many of the unwanted side effects caused by anti-tubulin drugs.

10

Perhaps the best known example of a highly successful anti-neoplastic drug that targets tubulin is provided by paclitaxel, and its marketed derivative, Taxol, from Bristol Meyers Squibb. Its applicability has indeed been seriously limited by difficulties in determining an adequate dosing regimen due to a range of problematic side effects. Taxol treatment has
15 resulted in anaphylaxis and severe hypersensitivity reactions characterised by dyspnea and hypotension requiring treatment, angioedema, and generalised urticaria in 2-4% of patients in clinical trials. All Taxol is administered after pretreatment with corticosteroids and despite pretreatment, fatal reactions have occurred. Severe conduction abnormalities resulting in life-threatening cardiac arrhythmia occur in less than 1 percent of patients and
20 must be treated by insertion of a pacemaker. Taxol can cause fetal harm or fetal death in pregnant women. Furthermore, administration is commonly accompanied by tachycardia, hypotension, flushing, skin reactions and shortness-of-breath (mild dyspnea).

Despite these shortcomings, Taxol has been hailed by many as the most successful new
25 anti-cancer therapeutic of the last three decades. Clearly, there is good justification for attempting to add to the list of mitotic inhibitors used to treat cancer. However, additional drugs that target tubulin or interfere with microtubule dynamics may be expected to have similar applicability and limitations as Taxol.

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The task of the present invention therefore is to find new potential target proteins/genes for therapeutical drugs other than tubulin that are essential for completion of mitosis. These proteins/genes may provide novel targets to screen for new anti-neoplastic or cytotoxic anti-cancer agents.

5

Unfortunately, until now, the systematic identification of such target proteins/genes using genetic screening methods has been difficult in metazoans, and has relied heavily on the use of the unicellular yeast. Several major advances in the use of certain metazoan model organisms, particularly the nematode worm *Caenorhabditis elegans*, have now begun to
10 offer new ways of bridging this gap.

The above-mentioned task of the invention to find new potential target proteins/genes for therapeutical drugs other than tubulin involved in mitosis processes is solved by a screening assay in *C. elegans* based on 'genomic RNA mediated interference (RNAi)'
15 combined with a highly probative microscopic assay for documenting the first rounds of embryonic cell division (Sulston *et al.*, The embryonic cell lineage of the nematode *Caenorhabditis elegans*. *Dev. Biol.* 100, 64-119 (1983); Gönczy *et al.*, Dissection of cell division processes in the one cell stage *Caenorhabditis elegans* embryo by mutational analysis. *J Cell Biol* 144, 927-946 (1999)). With this combination of techniques a selected
20 gene and also a variety of selected genes can be functionally characterized with unprecedented speed and efficiency.

The nematode *C. elegans* exhibits an almost entirely translucent body throughout its development, thereby offering unparalleled microscopic access for exquisitely detailed
25 cytological documentation, even for the earliest steps of embryogenesis. This important feature, along with its short life cycle (3-5 days), its ease of cultivation, and its low maintenance costs, has helped make *C. elegans* arguably the best studied of all metazoans. Also, sequence data are now available for over 97% of the *C. elegans* genome (*C. elegans* Sequencing Consortium. Genome sequence of the nematode *C. elegans*: a platform for
30 investigating biology. *Science* 282, 2012-2018 (1998)). Thus, *C. elegans* has proven to be

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an ideal organism for applying the new technique of RNA-mediated interference (RNAi). This technique consists in the targeted, sequence-specific inhibition of gene expression, as mediated by the introduction into an adult worm of double-stranded RNA (dsRNA) molecules corresponding to portions of the coding sequences of interest (Fire *et al.*, Potent and specific genetic interference by double-stranded RNA in *Caenorhabditis elegans*. *Nature* 391, 806-811 (1998)). For the vast majority of *C. elegans* genes tested to date, this has been shown to yield a sequence-specific inhibition of the targeted gene's expression, accompanied by clearly detectable loss of function phenotypes in the treated worm's F1 progeny (and even in some cases, in the treated worm itself).

A large-scale RNAi technique-based screen was performed for 2,232 (that means 96%) of the predicted open reading frames on chromosome III of *C. elegans* which is described in detail in Gönczy *et al.*, "Functional genomic analysis of cell division in *C. elegans* using RNAi of genes on chromosome III" *Nature* 408, 331-336 (2000). For the performance of this large-scale screen double-stranded RNA corresponding to the individual open reading frames was produced and micro-injected into adult *C. elegans* hermaphrodites, and the resulting embryos were analysed 24 hours later using time-lapse DIC microscopy.

Besides others, the *C. elegans* genes H38K22.2 (Genbank/EMBL ID: AL024499, provided in SEQ ID NO. 1 - 3), C02F5.1 (Genbank/EMBL ID: L14745; , provided in SEQ ID NO. 4 and 5) and F10E9.8 (GenBank/EMBL ID: L10986; provided in SEQ ID NO. 6 and 7) gave rise to a phenotype detectable by the DIC-assay implying a functional role of these genes in metazoan cell division processes.

In at least one case (for H38K22.2) it had also been possible to identify a structurally and functionally homologous gene, a so-called orthologous gene, in another species, in particular *Homo sapiens*, namely the human orthologue RP42.

For the mouse orthologue of the RP42 gene it had merely been known that the gene shows a strongly developmentally regulated expression, particularly in proliferating neuroblasts from which neocortical neurons originate (Mas *et al.*, "Cloning and expression of a novel gene, RP42, mapping to an autism susceptibility locus on 6Q16" *Genomics* 1; 65 (1), 70-74 (2000)). The functional role of RP42 in cell division and proliferation processes that

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makes it an excellent tool for the development or identification of drugs for diagnosis and/or therapy of proliferative diseases was not known so far.

With the essential function of said genes in cell division and proliferation known, these newly identified target genes and their corresponding gene products, any homologues, orthologues and derivatives thereof represent excellent tools for use in the development and isolation of a wide range of therapeutics including anti-proliferative agents and in the development of methods for diagnosis and treatment of proliferative diseases.

Therefore, in a first aspect, the present invention relates to isolated nucleic acid molecules encoding a polypeptide functionally involved in cell division and proliferation or a fragment thereof and comprising a nucleic acid sequence selected from the group consisting of:

- (a) the nucleic acid sequences presented in SEQ ID NO. 1 to 3, SEQ ID NO. 4 to 5, SEQ ID NO. 6 to 7, SEQ ID NO. 12 and fragments thereof and their complementary strands,
- (b) nucleic acid sequences encoding polypeptides that exhibit a sequence identity with SEQ ID NO. 8, SEQ ID NO. 9, SEQ ID NO. 10, SEQ ID NO. 11 or SEQ ID NO. 13 of at least 25 % over 100 residues and/or which are detectable in a computer aided search using the blast sequence analysis programs with an e-value of at most 10^{-30} ,
- (c) nucleic acid sequences which are capable of hybridizing with the nucleic acid sequences of (a) or (b) under conditions of medium stringency,
- (d) nucleic acid sequences which are degenerate as a result of the genetic code to any of the sequences defined in (a), (b) or (c).

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The above mentioned fragments of the isolated nucleic acid molecules may comprise a at least 15 nucleotides and preferably at least 20 nucleotides.

Additionally the above mentioned isolated nucleic acid molecules may be single or double-stranded DNA-molecules as well as single- or double-stranded RNA-molecules.

5

a):

The nucleic acid sequences of those nucleic acid molecules encoding a polypeptide functionally involved in cell division and proliferation as mentioned in a) are provided in the sequence listing

10 as SEQ ID NO. 1 - 3 (*C. elegans* genes H38K22.2 (Genbank/EMBL ID: AL024499)),
as SEQ ID NO. 4 and 5 (*C. elegans* gene C02F5.1 (Genbank/EMBL ID: L14745)),
as SEQ ID NO. 6 and 7 (*C. elegans* gene F10E9.8 (GenBank/EMBL ID: L10986)) and
as SEQ ID NO. 12 (the human H38K22.2 orthologue, the RP42 protein (NCBI Accession No. AF292100)).

15 The corresponding deduced amino acid sequences of these target genes are disclosed in SEQ ID NO. 8 (for H38K22.2a), in SEQ ID NO. 9 (for H38K22.2b), in SEQ ID NO. 10 (for C02F5.1), in SEQ ID NO. 11 (for F10E9.8) and in SEQ ID NO. 13 (for RP42).

b):

20 Additionally, the present invention also comprises isolated nucleic acid molecules that are structurally and functionally homologous counterparts (particularly orthologues) of at least one of said target genes as disclosed in SEQ ID NO 1 to 7 or 12.

Those homologous nucleic acid molecules may encode polypeptides that exhibit a sequence identity with SEQ ID NO. 8, SEQ ID NO. 9, SEQ ID NO. 10, SEQ ID NO. 11 or
25 SEQ ID NO. 13 of at least 25 % over 100 residues, preferably of at least 30 % over 100 residues, more preferably of at least 35 % over 100 residues and most preferably at least 40 % over 100 residues.

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Fig. 5 shows that the aforementioned sequence identities are significant homologies that are appropriate to identify a polypeptide as an orthologue of the target proteins as depicted in SEQ ID NO. 8 -11, and 13. Fig. 5 shows a multiple sequence alignment of the H38K22.2a family on protein level generated with a BLAST sequence analysis program. In this alignment the two *C. elegans* splice variants H38K22.2a and H38K22.2b are compared to their corresponding orthologues in *Drosophila* (CG7427), in mouse (AAF04863) and in *Homo sapiens* (AAH09478). The statistics in Fig 5 for the alignments show that the sequence identity on protein level between the *C. elegans* clone H38K22.2a and its human orthologue (AAH09478) is 36 % over 299 residues. Similarly, the sequence identities between *C. elegans* clone H38K22.2b (the other splice variant) and its human orthologue is 36 % over 238 residues. It is obvious to anyone skilled in the art that these sequence homologies are significant homologies and that therefore the human clone with the accession No. AAH09478 is unambiguously identified as the human orthologue of the *C. elegans* clones H38K22.2a and H38K22.2b.

The invention also comprises isolated nucleic acid molecules that are detectable in a computer aided search using one of the BLAST sequence analysis programs with an e-value of at most 10^{-30} , preferably with an e-value of at most 10^{-35} , more preferably with an e-value of at most 10^{-40} .

Fig. 5 shows that the aforementioned e-values characterize significant sequence homologies that are appropriate to identify a polypeptide as an orthologue of the target proteins as depicted in SEQ ID NO. 8 -11, and 13.

The BLAST sequence analysis programs are programs used for sequence analysis that are publically available and known to anyone skilled in the art. When sequence alignments are done by a BLAST sequence analysis program, most of those programs calculate so called "e-values" to characterize the grade of homology between the compared sequences. Generally a small e-value characterizes a high sequence identity / homology, whereas larger e-values characterize lower sequence identities / homologies.

"Homology" means the degree of identity between two known sequences. As stated above, homologies, that means sequence identities, may suitably be determined by means of computer programs known in the art. The degree of homology required for the sequence variant will depend upon the intended use of the sequence. It is well within the capability

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of a person skilled in the art to effect mutational, insertional and deletional mutations which are designed to improve the function of the sequence or otherwise provide a methodological advantage.

5 c):

The present invention further relates to isolated nucleic acid sequences or fragments thereof which are capable of hybridizing with the nucleic acid sequences of (a) or (b) under conditions of medium/high stringency.

10 The grade of sequence identity between a first and a second nucleic acid molecule can also be characterized by the capability of the first nucleic acid molecule to hybridize under certain conditions to a second nucleic acid molecule.

Suitable experimental conditions for determining whether a given DNA or RNA sequence "hybridizes" to a specified polynucleotide or oligonucleotide probe involve presoaking of the filter containing the DNA or RNA to examine for hybridization in 5 x SSC (sodium chloride/sodium citrate) buffer for 10 minutes, and prehybridization of the filter in a
15 solution of 5 x SSC, 5 x Denhardt's solution, 0,5 % SDS and 100 mg/ml of denaturated sonicated salmon sperm DNA (Maniatis et al., 1989), followed by hybridization in the same solution containing a concentration of 10 ng/ml of a random primed (Feinberg, A.P. and Vogelstein, B. (1983), *Anal. Biochem.* 132:6-13), ³²P-dCTP-labeled (specific activity > 1 x
20 10⁹ cpm/μg) probe for 12 hours at approximately 45°C. The filter is then washed twice for 30 minutes in 2 x SSC, 0,5% SDS at at least 55°C (low stringency), at least 60°C (medium stringency), preferably at least 65°C (medium/high stringency), more preferably at least 70°C (high stringency) or most preferably at least 75°C (very high stringency). Molecules to which the probe hybridizes under the chosen conditions are detected using an x-ray film.

25

d):

The present invention further relates to isolated nucleic acid molecules or fragments thereof which are degenerate as a result of the genetic code to any of the sequences defined in (a), (b) or (c).

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The application of automated gene synthesis provides an opportunity for generating sequence variants of the naturally occurring genes. It will be appreciated, for example, that polynucleotides coding for the same gene products can be generated by substituting synonymous codons for those represented in the naturally occurring polynucleotide sequences as identified herein. Such sequences will be referred to as “degenerate” to the naturally occurring sequences. In addition, polynucleotides coding for synthetic variants of the corresponding amino acid sequences can be generated which, for example, will result in one or more amino acids substitutions, deletions or additions. Also, nucleic acid molecules comprising one or more synthetic nucleotide derivatives (including morpholinos) which provide said nucleotide sequence with a desired feature, e.g. a reactive or detectable group, can be prepared. Synthetic derivatives with desirable properties may also be included in the corresponding polypeptides. All such derivatives and fragments of the above identified genes and gene products showing at least part of the biological activity of the naturally occurring sequences or which are still suitable to be used, for example, as probes for, e.g. identification of homologous genes or gene products, are included within the scope of the present invention.

Having herein provided the nucleotide sequences of various genes functionally involved in cell division and proliferation, it will be appreciated that automated techniques of gene synthesis and/or amplification may be used to isolate said nucleic acid molecules *in vitro*. Because of the length of some coding sequences, application of automated synthesis may require staged gene construction, in which regions of the gene up to about 300 nucleotides in length are synthesized individually and then ligated in correct succession for final assembly. Individually synthesized gene regions can be amplified prior to assembly, using polymerase chain reaction (PCR) technology. The technique of PCR amplification may also be used to directly generate all or part of the final genes/nucleic acid molecules. In this case, primers are synthesized which will be able to prime the PCR amplification of the final product, either in one piece or in several pieces that may be ligated together. For this purpose, either cDNA or genomic DNA may be used as the template for the PCR amplification. The cDNA template may be derived from commercially available or self-constructed cDNA libraries.

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In a second aspect, the invention relates to nucleic acid probes comprising a nucleic acid sequence as previously characterized under (a) to (d) which may be a polynucleotide or an oligonucleotide comprising at least 15 nucleotides containing a detectable label.

These nucleic acid probes may be synthesized by use of DNA synthesizers according to standard procedures or, preferably for long sequences, by use of PCR technology with a
5 selected template sequence and selected primers. In the use of the nucleotide sequences as probes, the particular probe may be labeled with any suitable label known to those skilled in the art, including radioactive and non-radioactive labels. Typical radioactive labels include ^{32}P , ^{125}I , ^{35}S , or the like. A probe labeled with a radioactive isotope can be
10 constructed from a DNA template by a conventional nick translation reaction using a DNase and DNA polymerase. Non-radioactive labels include, for example, ligands such as biotin or thyroxine, or various luminescent or fluorescent compounds. The probe may also be labeled at both ends with different types of labels, for example with an isotopic label at one end and a biotin label at the other end. The labeled probe and sample can then be
15 combined in a hybridization buffer solution and held at an appropriate temperature until annealing occurs.

The invention also includes an assay kit comprising either an isolated nucleic acid molecule as defined above or a fragment thereof or a probe as defined above in a suitable
20 container.

Duplex formation and stability depend on substantial complementarity between the two strands of a hybrid and a certain degree of mismatch can be tolerated. Therefore, the nucleic acid molecules and probes of the present invention may include mutations (both single and multiple), deletions, insertions of the above identified sequences, and
25 combinations thereof, as long as said sequence variants still have substantial sequence homology to the original sequence which permits the formation of stable hybrids with the target nucleotide sequence of interest.

The above identified nucleic acid molecules and probes coding for polypeptides
30 functionally involved in cell division and proliferation or a part thereof will have a wide range of useful applications, including their use for identifying homologous, in particular orthologous, genes in the same or different species, their use in screening assays for

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identification of interacting drugs that inhibit, stimulate or effect cell division or proliferation, their use for developing computational models, structural models or other models for evaluating drug binding and efficacy, and their diagnostic or therapeutic use for detection or treatment of diseases associated with anomalous and/or excessive cell division
5 or proliferation, in particular neoplastic diseases, including both solid tumors and hemopoietic cancers, or coronary restenosis. Exemplary neoplastic diseases include carcinomas, such as adenocarcinomas and melanomas; mesodermal tumors, such as neuroblastomas and retinoblastomas; sarcomas and various leukemias; and lymphomas. Of particular interest are tumors of the breast, ovaries, gastrointestinal tract, liver, lung,
10 thyroid glands, prostate gland, brain, pancreas, urinary tract, and salivary glands. Still more specific, tumors of the breast, ovaries, lung, colon, and lymphomas are contemplated.

In a third aspect, the present invention relates to the use of the above identified nucleic acid
15 molecules and probes for diagnostic purposes. This diagnostic use of the above identified nucleic acid molecules and probes may include, but is not limited to the quantitative detection of the expression of said target genes in biological probes (preferably, but not limited to cell extracts, body fluids, etc.), particularly by quantitative hybridization to the endogenous nucleic acid molecules comprising the above-characterized nucleic acid
20 sequences (particularly cDNA, RNA). An abnormal and/or excessive expression of said target genes involved in cell division may be diagnosed that way.

In a forth aspect, the present invention relates to the use of the above identified nucleic acid molecules, probes or their corresponding polypeptides for therapeutical purposes.

25

This therapeutical use of the above identified nucleic acid molecules, probes or their corresponding polypeptides may include, but is not limited to the use of said nucleic acid molecules and their corresponding polypeptides for direct or indirect inhibition of the expression of said target genes and/or for inhibition of the function of said target genes.

30 Particularly gene therapy vectors, e.g. viruses, or naked or encapsulated DNA or RNA (e.g. an antisense nucleotide sequence) with the above-identified sequences might be suitable

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for the introduction into the body of a subject suffering from a proliferative disease or from a disease affecting cell division for therapeutical purposes.

A particularly preferred therapeutical use of the above identified nucleic acid molecules or
5 probes relates to their use in a therapeutical application of the RNAi technique, particularly in humans or in human cells.

Double-stranded RNA oligonucleotides effect silencing of the expression of gene(s) which are highly homologous to either of the RNA strands in the duplex. Recent discoveries reveal that this effect, called RNA interference (RNAi), that had been originally discovered
10 in *C. elegans*, can also be observed in cells, particularly in human cells. Therefore the invention further comprises the use of double-stranded RNA oligonucleotides with the above identified nucleotide sequences (as stated in a) to d)), preferably with a length of at least 15 nucleotides (nt), more preferably with a length of at least 20 nt, for therapeutical silencing of the expression of genes involved in cell division or proliferation in cells of
15 other species, particularly in human cells. This therapeutical use particularly applies to cells of an individual that suffers from a disease associated with anormalous and/or excessive cell division or proliferation, particularly a coronary restinosis or a neoplastic disease selected from the group consisting of lymphoma, lung cancer, colon cancer, ovarian cancer and breast cancer.

20

In a fifth aspect, the invention further comprises a nucleic acid construct or a recombinant vector having incorporated the nucleic acid molecules as defined in (a) to (d) or a fragment thereof.

“Nucleic acid construct“ is defined herein as any nucleic acid molecule, either single- or
25 double-stranded, in which nucleic acid sequences are combined and juxtaposed in a manner which will not occur naturally. The vector may be any vector which can be conveniently subjected to recombinant DNA procedures. The choice of the vector will usually depend on the host cell into which it is to be introduced. The vector may be an extrachromosomal entity, the replication of which is independent of chromosomal
30 replication, e.g. a plasmid. Alternatively, the vector may be one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with the chromosome(s) into which it has been integrated.

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The vector is preferably an expression vector in which the nucleic acid molecule as defined in (a) to (d) or a fragment thereof is operably linked to heterologous or homologous control sequences. The term "control sequences" is defined herein to include all components
5 which are necessary or advantageous for expression of the coding nucleic acid sequence. Such control sequences include, but are not limited to, a promoter, a ribosome binding site, translation initiation and termination signals and, optionally, a repressor gene or various activator genes. Control sequences are referred to as "homologous" if they are naturally linked to the coding nucleic acid sequence of interest and referred to as "heterologous" if
10 this is not the case. The term "operably linked" indicates that the sequences are arranged so that they function in concert for their intended purpose, i.e. expression of the desired protein.

The promoter may be any DNA sequence which shows transcriptional activity in the host
15 cell of choice and may be derived from genes encoding proteins either homologous or heterologous to the host cell.

Examples of suitable promoters for directing the transcription in a bacterial host are, e.g., the phage Lambda P_R or P_L promoters, the *lac*, *trp* or *tac* promoters of *E. coli*, the promoter
20 of the *Bacillus subtilis* alkaline protease gene or the *Bacillus licheniformis* alpha-amylase gene.

Examples of suitable promoters for directing the transcription in mammalian cells are, e.g., the SV40 promoter (Subramani et al., *Mol. Cell. Biol.* 1 (1981), 854-864), the MT-1
25 (metallothionein gene) promoter (Palmiter et al., *Science* 222 (1983), 809-814) or the adenovirus 2 major late promoter.

Examples of suitable promoters for use in insect cells are, e.g., the polyhedrin promoter (Vasuvedan et al., *Febs. Lett* 311, (1992), 7-11), the *Autographa californica* polyhedrosis
30 basic protein promoter (EP 397 485), or the baculovirus immediate early gene 1 promoter (US 5,155,037, US 5,162,222).

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Examples of suitable promoters for use in yeast cells include promoters from yeast glycolytic genes (Hitzeman et al., *J. Biol. Chem.* 255 (1980), 1203-12080; Alber and Kawasaki, *J. Mol. Appl. Gen.* 1 (1982), 419-434) and the ADH2-4c promoter (Russell et al., *Nature* 304 (1983), 652-654).

5

The coding sequence may, if necessary, be operably linked to a suitable terminator, such as the human growth hormone terminator (Palmiter et al., *Science* 222, 809-814 (1983)), or a polyadenylation sequence. Also, to permit secretion of the expressed protein, a signal sequence may precede the coding sequence.

10

Further, the vector may comprise a DNA sequence enabling the vector to replicate in the host cell in question. Examples of such sequences are the origins of replication of the plasmids pUC19, pACYC177, pUB110, pE194, pAMB1 and pIJ702. Another example of such a sequence (when the host cell is a mammalian cell) is the SV40 origin of replication.

15

When the host cell is a yeast cell, suitable sequences enabling the vector to replicate are the yeast plasmid 2 μ replication genes REP 1-3 and origin of replication.

20

The vector may also comprise a selectable marker, e.g. a gene coding for a product which complements a defect in the host cell, such as the gene coding for dihydrofolate reductase (DHFR) or a gene which confers resistance to a drug, e.g. ampicillin, kanamycin, tetracyclin, chloramphenicol, neomycin or hygromycin.

25

A number of vectors suitable for expression in prokaryotic or eukaryotic cells are known in the art and several of them are commercially available. Some commercially available mammalian expression vectors which may be suitable include, but are not limited to, pMC1neo (Stratagene), pXT1 (Stratagene), pSG5 (Stratagene), pcDNAI (Invitrogen), EBO-pSV2-neo (ATCC 37593), pBPV-1(8-2) (ATCC 37110), pSV2-dhfr (ATCC 37146).

30

In a sixth aspect, the invention comprises host cells into which the nucleic acid construct or the recombinant vector is introduced. These host cells may be prokaryotic or eukaryotic, including, but not limited to, bacteria, fungal cells, including yeast and filamentous fungi,

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mammalian cells, including, but not limited to, cell lines of human, bovine, porcine, monkey and rodent origin, and insect cells including, but not limited to, drosophila derived cell lines.

- 5 The selection of an appropriate host cell will be dependent on a number of factors recognized by the art. These include, e.g., compatibility with the chosen vector, toxicity of the (co)products, ease of recovery of the desired protein or polypeptide, expression characteristics, biosafety and costs.

Examples of suitable prokaryotic cells are gram positive bacteria such as *Bacillus subtilis*,
10 *Bacillus licheniformis*, *Bacillus brevis*, *Streptomyces lividans* etc. or gram negative bacteria such as *E. coli*.

The yeast host cell may be selected from a species of *Saccharomyces* or *Schizosaccharomyces*, e.g. *Saccharomyces cerevisiae*. Useful filamentous fungi may be selected from a species of *Aspergillus*, e.g. *Aspergillus oryzae* or *Aspergillus niger*.

- 15 Cell lines derived from mammalian species which may be suitable and which are commercially available include, but are not limited to, COS-1 (ATCC CRL 1650) COS-7 (ATCC CRL 1651), CHO-K1 (ATCC CCL 61), 3T3 (ATCCL 92), NIH/3T3 (ATCC CRL 1658), HeLa (ATCCL 2), and MRC-5 (ATCC CCL 171).

- 20 The recombinant vector may be introduced into the host cells according to any one of a number of techniques including, but not limited to, transformation, transfection, protoplast fusion, and electroporation.

The recombinant host cells are then cultivated in a suitable nutrient medium under
25 conditions permitting the expression of the protein of interest. The medium used to cultivate the cells may be any conventional medium suitable for growing the host cells, such as minimal or complex media containing appropriate supplements. Suitable media are available from commercial suppliers or may be prepared according to published recipes (e.g. in catalogues of the American Type Culture Collection).

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Identification of the heterologous polypeptide expressing host cell clones may be done by several means, including, but not limited to, immunological reactivity with specific antibodies.

5 In a seventh aspect, the invention is related to a method for producing a polypeptide functionally involved in cell division and proliferation or a fragment thereof in a host cell comprising the steps

- (i) transferring the expression vector with an operably linked nucleic acid molecule as defined in (a) to (d) into a suitable host cell, and
- 10 (ii) cultivating the host cells of step (i) under conditions which will permit the expression of said polypeptide or fragment thereof and
- (iii) optionally, secretion of the expressed polypeptide into the culture medium.

In an eighth aspect, the invention comprises a polypeptide functionally involved in cell
15 division and proliferation or a fragment thereof comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequences depicted in SEQ ID NO. 8, 9, 10, 11 and 13 and fragments thereof,
- (b) amino acid sequences which exhibit a sequence identity with the sequences of
20 (a) of at least 25 % over 100 residues, preferably of at least 30 % over 100 residues, more preferably of at least 35 % over 100 residues and most preferably of at least 40 % over a 100 residues and/or which are detectable in a computer aided search using the BLAST sequence analysis programs with an e-value of at most 10^{-30} , preferably with an e-value of at most 10^{-35} and most
25 preferably with an e-value of at most 10^{-40} ,
- (c) amino acid sequences encoded by a nucleic acid molecule that is capable of hybridizing with the nucleic acid sequences of (a) or (b) or encoded by a nucleic acid molecule that is degenerate as a result of the genetic code to any of the sequences as defined in (a) or (b).

The heterologous polypeptide may also be a fusion polypeptide in which another polypeptide is fused at the N-terminus or the C-terminus of the polypeptide of interest or fragment thereof. A fused polypeptide is produced by fusing a nucleic acid sequence (or a portion thereof) encoding another polypeptide to a nucleic acid sequence (or a portion thereof) of the present invention. Techniques for producing fusion polypeptides are known in the art and include ligating the coding sequences so that they are in frame and the expression of the fusion polypeptide is under control of the same promotor(s) and terminator.

Expression of the polypeptides of interest may also be performed using *in vitro* produced synthetic mRNA. Synthetic mRNA can be efficiently translated in various cell-free systems, including but not limited to, wheat germ extracts and reticulocyte extracts, as well as efficiently translated in cell based systems including, but not limited to, microinjection into frog oocytes, preferably *Xenopus* oocytes.

In a ninth aspect, the invention involves antibodies against the above identified polypeptides and against immunogenic fragments thereof. The term "antibody" as used herein includes both polyclonal and monoclonal antibodies, as well as fragments thereof, such as Fv, Fab and F(ab)₂ fragments that are capable of binding antigen or hapten. The present invention also contemplates "humanized" hybrid antibodies wherein amino acid sequences of a non-human donor antibody exhibiting a desired antigen-specificity are combined with sequences of a human acceptor antibody. The donor sequences will usually include at least the antigen-binding amino acid residues of the donor but may comprise other structurally and/or functionally relevant amino acid residues of the donor antibody as well. Such hybrids can be prepared by several methods well known in the art (see e.g. WO 89/09622; WO 94/11509; Couto, *Hybridoma* 13 (1994), 215-219; Presta, *Cancer Research* 57 (1997), 4593-4599). The antibodies of the present invention will have a wide range of useful applications, including their use for affinity purification of the corresponding immunogenic (poly)peptides, their use for the preparation of anti-idiotypic antibodies, as well as their use as specific binding agents in various assays, e.g. diagnostic or drug-screening assays, or in a method for treatment of diseases associated with anomalous and/or excessive cell division or proliferation as exemplified above. Specifically, said

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antibodies or suitable fragments thereof, particularly in humanized form, may be used as therapeutic agents in a method for treating cancer and other diseases associated with anomalous and/or excessive cell division or proliferation as exemplified above. Also, antibodies may be raised to the most characteristic parts of the above identified polypeptides and subsequently be used to identify structurally and/or functionally related polypeptides from other sources as well as mutations and derivatives of the above identified polypeptides.

To raise antibodies against the polypeptides of the present invention, there may be used as an immunogen either the intact polypeptide or an immunogenic fragment thereof, produced in a suitable host cell as described above or by standard peptide synthesis techniques.

Polyclonal antibodies are raised by immunizing animals, such as mice, rats, guinea pigs, rabbits, goats, sheep, horses etc., with an appropriate concentration of the polypeptide or peptide fragment of interest either with or without an immune adjuvant.

Acceptable immune adjuvants include, but are not limited to, Freund's complete adjuvant, Freund's incomplete adjuvant, alum-precipitate, water-in-oil-emulsion containing *Corynebacterium parvum* and tRNA.

In a typical immunization protocol each animal receives between about 0,1 µg and about 1000 µg of the immunogen at multiple sites either subcutaneously (SC), intraperitoneally (IP), intradermally or in any combination thereof in an initial immunization. The animals may or may not receive booster injections following the initial injection. Those animals receiving booster injections are generally given an equal amount of the immunogen in Freund's incomplete adjuvant by the same route at intervals of about three or four weeks until maximal titers are obtained. At about 7-14 days after each booster immunization or about weekly after a single immunization, the animals are bled, the serum collected, and aliquots are stored at about -20°C.

Monoclonal antibodies which are reactive with the polypeptide or peptide fragment of interest are prepared using basically the technique of Kohler and Milstein, Nature 256: 495-497 (1975). First, animals, e.g. Balb/c mice, are immunized using a protocol similar to that described above. Lymphocytes from antibody-positive animals, preferably

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splenocytes, are obtained by removing spleens from immunized animals by standard procedures known in the art. Hybridoma cells are produced by mixing the splenocytes with an appropriate fusion partner, preferably myeloma cells, under conditions which will allow the formation of stable hybridomas. Fusion partners may include, but are not limited to:

5 mouse myelomas P3/NS1/Ag 4-1; MPC-11; S-194 and Sp 2/0. Fused hybridoma cells are selected by growth in a selection medium and are screened for antibody production. Positive hybridomas may be grown and injected into, e.g., pristane-primed Balb/c mice for ascites production. Ascites fluid is collected about 1-2 weeks after cell transfer and the monoclonal antibodies are purified by techniques known in the art. Alternatively, *in vitro*

10 production of monoclonal antibodies (mAb) is possible by cultivating the hybridomas in a suitable medium, e.g. DMEM with fetal calf serum, and recovering the mAb by techniques known in the art.

Recovered antibody can then be coupled covalently to a detectable label, such as a radiolabel, enzyme label, luminescent label, fluorescent label or the like, using linker

15 technology established for this purpose.

Antibody titers of ascites or hybridoma culture fluids are determined by various serological or immunological assays which include, but are not limited to, precipitation, passive agglutination, enzyme-linked immunosorbent antibody (ELISA) technique and radioimmunoassay techniques. Similar assays may be used to detect the presence of the

20 above identified polypeptides or fragments thereof in body fluids or tissue and cell extracts.

Assay kits for performing the various assays mentioned in the present application may comprise suitable isolated nucleic acid or amino acid sequences of the above identified genes or gene products, labelled or unlabelled, and/or specific ligands (e.g. antibodies)

25 thereto and auxiliary reagents as appropriate and known in the art. The assays may be liquid phase assays as well as solid phase assays (i.e. with one or more reagents immobilized on a support).

Unless otherwise specified, the manipulations of nucleic acids and polypeptides/-proteins can be performed using standard methods of molecular biology and immunology (see, e.g.

30 Maniatis et al. (1989), Molecular cloning: A laboratory manual, Cold Spring Harbor Lab., Cold Spring Harbor, NY; Ausubel, F.M. et al. (eds.) "Current protocols in Molecular

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Biology". John Wiley and Sons, 1995; Tijssen, P., Practice and Theory of Enzyme Immunoassays, Elsevier Press, Amsterdam, Oxford, New York, 1985).

5 The invention further includes an assay kit comprising either the polypeptide as defined above or a fragment thereof or an antibody against said polypeptides as defined above or against immunogenic fragments thereof.

10 These recombinant polypeptides or fragments thereof as well as antibodies against those polypeptides or immunogenic fragments thereof will have a wide range of useful applications, including their use in screening assays for interacting drugs that inhibit, stimulate or effect the cell division or proliferation, their use for developing computational models, structural models or other models for evaluating drug binding and efficacy, and their use in a method for diagnosis or treatment of diseases associated with anomalous and/or excessive cell division or proliferation, in particular neoplastic diseases, including
15 both solid tumors and hemopoietic cancers, or coronary restenosis. Exemplary neoplastic diseases include carcinomas, such as adenocarcinomas and melanomas; mesodermal tumors, such as neuroblastomas and retinoblastomas; sarcomas and various leukemias; and lymphomas. Of particular interest are tumors of the breast, ovaries, gastrointestinal tract, liver, lung, thyroid glands, prostate gland, brain, pancreas, urinary tract, and salivary
20 glands. Still more specific, tumors of the breast, ovaries, lung, colon, and lymphomas are contemplated.

Therefore in a tenth aspect, the present invention explicitly includes the use of polypeptides as defined above or fragments thereof or of antibodies against said
25 polypeptides or immunogenic fragments thereof in a screening assay for interacting drugs that inhibit, stimulate or effect the cell division or proliferation.

Such a screening assay for interacting drugs may particularly comprise, but is not limited to the following steps:

30

1. recombinant expression of said polypeptide or of an appropriate derivative thereof

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2. isolation and optionally purification of the recombinantly expressed polypeptide or of its derivative, in particular by affinity chromatography
3. optionally labelling of the chemical compounds that are tested to interact with said polypeptide or its derivative and/or labelling of the recombinantly expressed polypeptide
4. immobilization of the recombinantly expressed polypeptide or of its derivative to a solid phase
5. binding of a potential interaction partner or a variety thereof to the immobilized polypeptide or its derivative
6. optionally one or more washing steps
7. detection and/or quantification of the interaction, in particular by monitoring the amount of label remaining associated with the solid phase over background levels.

Step 1 includes the recombinant expression of the above identified polypeptide or of its derivative from a suitable expression system, in particular from cell-free translation, bacterial expression, or baculovirus-based expression in insect cells.

Step 2 comprises the isolation and optionally the subsequent purification of said recombinantly expressed polypeptides with appropriate biochemical techniques that are familiar to a person skilled in the art.

Alternatively, these screening assays may also include the expression of derivatives of the above identified polypeptides which comprises the expression of said polypeptides as a fusion protein or as a modified protein, in particular as a GST-fusion protein or as a protein bearing a so called "tag"-sequence. These "tags"-sequences consist of short nucleotide sequences that are ligated 'in frame' either to the N- or to the C-terminal end of the coding region of said target gene. One of the most common tags that are used to label recombinantly expressed genes is the poly-Histidine-tag which encodes a homopolypeptide consisting merely of histidines. In this context the term "polypeptide" does not merely comprise polypeptides with the nucleic acid sequences of SEQ ID No. 1 bis 7, their naturally occurring homologues, preferably orthologues, more preferably human orthologues, in particular the RP42 gene (SEQ ID No. 12), but also derivatives of these polypeptides, in particular fusion proteins or polypeptides comprising a tag-sequence.

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These polypeptides, particularly those labelled by an appropriate tag-sequence (for instance a His-tag) or by GST, may be purified by standard affinity chromatography protocols, in particular by using chromatography resins linked to anti-His-tag-antibodies or to anti-GST-antibodies which are both commercially available. Alternatively to the use of
5 anti-tag- or anti-GST-antibodies or other 'label-specific' antibodies the purification may also involve the use of antibodies against said polypeptides. Screening assays that involve a purification step of the recombinantly expressed target genes as described above (step 2) are preferred embodiments of this aspect of the invention.

In a third - optional - step the compounds tested for interaction may be labelled by
10 incorporation of radioactive isotopes or by reaction with luminescent or fluorescent compounds. Alternatively or additionally also the recombinantly expressed polypeptide may be labelled.

In a forth step the recombinantly expressed polypeptide is immobilized to a solid phase, particularly (but not limited) to a chromatography resin. The coupling to the solid phase is
15 thereby preferably established by the generation of covalent bonds.

In a fifth step a candidate chemical compound that might be a potential interaction partner of the said recombinant polypeptide or a complex variety thereof (particularly a drug library) is brought into contact with the immobilized polypeptide.

In a sixth - optional - step one or several washing steps may be performed. As a result just
20 compounds that strongly interact with the immobilized polypeptide remain bound to the solid (immobilized) phase.

In step 7 the interaction between the polypeptide and the specific compound is detected, in particular by monitoring the amount of label remaining associated with the solid phase over background levels.

25

Brief Description of the Drawings

Fig. 1 shows DIC microscopy images taken from time-lapse recording of the first two rounds of embryonic cell division in wild type *C. elegans*.

Fig. 2 shows DIC microscopy images taken from time-lapse recording of the first two
30 rounds of embryonic cell division in *C. elegans* F1 progeny from F0 parent treated with ds RNA "300C3" or "340G12" directed against gene H38K22.2.

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Fig. 3 shows DIC microscopy images taken from time-lapse recording of the first two rounds of embryonic cell division in *C. elegans* F1 progeny from F0 parent treated with dsRNA "307C1" directed against gene C02F5.1.

Fig. 4 shows shows DIC microscopy images taken from time-lapse recording of the first two rounds of embryonic cell division in *C. elegans* F1 progeny from F0 parent treated with ds RNA "305A12" directed against gene F10E9.8.

Fig 5 shows a multiple sequence alignment of the H38K22.2a family. Herein, the amino acid sequences of the two *C. elegans* splice variants H38K22.2a and H38K22.2b are compared to the amino acid sequences of their orthologues in *Drosophila* (CG7427), in mouse (AAF04863) and in homo sapiens (AAH09478).

The "statistics" refer to values that characterize the grade of homology between the individual sequences, as the e-value, the sequence identities and the conservatively changed residues (positives).

15

Description of the sequence protocol:

- | | | |
|----|--------------|--|
| 15 | SEQ ID NO. 1 | shows the unspliced DNA sequence common to both isoforms a and b of the <i>C. elegans</i> gene H38K22.2 (3104 bp). |
| 20 | SEQ ID NO. 2 | shows the spliced DNA sequence of the <i>C. elegans</i> gene H38K22.2a isoform (1011 bp). |
| | SEQ ID NO. 3 | shows the spliced DNA sequence of the <i>C. elegans</i> gene H38K22.2b isoform (852 bp). |
| | SEQ ID NO. 4 | shows the unspliced DNA sequence of the <i>C. elegans</i> gene C02F5.1 (3308 bp). |
| 25 | SEQ ID NO. 5 | shows the spliced DNA sequence of the <i>C. elegans</i> gene C02F5.1 (3033 bp). |
| | SEQ ID NO. 6 | shows the unspliced DNA sequence of the <i>C. elegans</i> gene F10E9.8 |

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(7097 bp).

SEQ ID NO. 7 shows the spliced DNA sequence of the *C. elegans* gene F10E9.8 (3624 bp).

5 SEQ ID NO. 8 shows the deduced amino acid sequence of the *C. elegans* gene H38K22.2a isoform (336 aa).

SEQ ID NO. 9 shows the deduced amino acid sequence of the *C. elegans* gene H38K22.2b isoform (283 aa).

SEQ ID NO. 10 shows the deduced amino acid sequence of the *C. elegans* gene C02F5.1 (1010 aa).

10 SEQ ID NO. 11 shows the deduced amino acid sequence of the *C. elegans* gene F10E9.8 (1207 aa).

SEQ ID NO. 12 shows the cDNA sequence of a human orthologue of H38K22.2 (780 bp).

15 SEQ ID NO. 13 shows the deduced amino acid sequence of a human orthologue of H38K22.2 (260 aa).

20 The following examples illustrate the present invention without, however, limiting the same thereto.

EXAMPLE 1: Generation of dsRNA molecules for RNAi experiments

25 First, oligonucleotide primer pair sequences were selected to amplify portions of the gene of interest's coding region using standard PCR techniques. Primer pairs were chosen to yield PCR products containing at least 500 bases of coding sequence, or a maximum of

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coding bases for genes smaller than 500 bases. In order to permit the subsequent use of the PCR product as a template for *in vitro* RNA transcription reactions from both DNA strands, the T7 polymerase promoter sequence "TAATACGACTCACTATAGG" was added to the 5' end of forward primers, and the T3 polymerase promoter sequence
5 "AATTAACCCTCACTAAAGG" was added to the 5' end of reverse primers. The synthesis of oligonucleotide primers was completed by a commercial supplier (Sigma-Genosys, UK or MWG-Biotech, Germany).

PCR reactions were performed in a volume of 50 μ l, with Taq polymerase using 0.8 μ M primers and approximately 0.1 μ g of wild-type (N2 strain) genomic DNA template. The
10 PCR products were EtOH precipitated, washed with 70% EtOH and resuspended in 7.0 μ l TE. 1.0 μ l of the PCR reaction was pipetted into each of two fresh tubes for 5 μ l transcription reactions using T3 and T7 RNA polymerases. The separate T3 and T7 transcription reactions were performed according to the manufacturer's instructions (Ambion, Megascript kit), each diluted to 50 μ l with RNase-free water and then combined.
15 The mixed RNA was purified using RNeasy kits according to the manufacturer's instructions (Qiagen), and eluted into a total of 130 μ l of RNase-free H₂O. 50 μ l of this was mixed with 10 μ l 6X injection buffer (40 mM KPO₄ pH 7.5, 6 mM potassium citrate, pH 7.5, 4% PEG 6000). The RNA was annealed by heating at 68°C for 10 min, and at 37°C for 30 min. Concentration of the final dsRNAs were measured to be in the range of 0.1-0.3
20 μ g/ μ l. The products of the PCR reaction, of the T3 and T7 transcription reactions, as well as the dsRNA species were run on 1% agarose gels to be examined for quality control purposes. Success of double stranding was assessed by scoring shift in gel mobility with respect to single stranded RNA, when run on non-denaturing gels.

25

EXAMPLE 2: Injections of dsRNA and phenotypic assays

dsRNAs were injected bilaterally into the syncitial portion of both gonads of wild-type (N2 strain) young adult hermaphrodites, and the animals incubated at 20°C for 24 hrs.
30 Embryos were then dissected out from the injected animals and analyzed by time-lapse

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differential interference contrast videomicroscopy for potential defects in cell division processes, capturing 1 image every 5 seconds, as previously described (Gönczy *et al.*, Dissection of cell division processes in the one cell stage *Caenorhabditis elegans* embryo by mutational analysis. *J Cell Biol* 144, 927-946 (1999)). For each experiment, embryos
5 from at least 3 different injected worms were filmed in this manner, from shortly after fertilization until the four cell stage. Embryos from 2 additional injected worms were also recorded via still images, thus yielding phenotypic documentation for at least 5 injected worms in each experiment.

In some cases, embryos exhibited acute sensitivity to osmotic changes, as evidenced by
10 their loss of structural integrity during the dissection of the injected animals. In order to overcome this limitation, injected animals were not dissected, but rather, anaesthetized for 10 min in M9 medium containing 0.1% tricaine and 0.01% tetramisole, and mounted intact on an agarose pad to observe the F1 embryogenesis *in utero* (Kirby *et al.*, *Dev. Biol.* 142, 203-215 (1990)). The resolution achieved by viewing through the body wall does not equal
15 that achieved by observing dissected embryos, and only limited phenotypic analysis was conducted in these cases.

Three injected animals were also transferred to a fresh plate 24 hrs after injection of dsRNA, and left at 20°C. Two days later, the plate was checked with a stereomicroscope (20-40x total magnification) for the presence of F1 larvae (L2's-L4's), as well as their
20 developmental stage. Two days after that, the plate was inspected again for the presence of F1 adults, as well as their overall body morphology and the presence of F2 progeny.

EXAMPLE 3: Characterization of the *C. elegans* gene H38K22.2

25 Two dsRNAs, "300C3" and "340G12", were designed and used to specifically silence the expression of the *C. elegans* gene H38K22.2 by RNAi, thereby testing its functional involvement in the first 2 rounds of embryonic cell division in this metazoan species. The dsRNAs were synthesized *in vitro* from PCR-amplified wild type genomic DNA fragments
30 of the H38K22.2 gene. For the PCR, two sets of primer pairs were used:

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"TCAATCAGTATGTGACCC" with "GGAAGAAATTGGGGAAACA" as forward and reverse primers, respectively, to generate dsRNA "300C3", and "ATCGAGCGCCTCTTCAATC" with "TGGTGTCTCCATTTGCTGA" as forward and reverse primers, respectively, to generate dsRNA "340G12". The dsRNAs were purified, and injected into adult hermaphrodite worms. The phenotypic consequences of the RNAi treatment were documented 24 hours later in the F1 progeny of injected worms, using time-lapse differential interference contrast (DIC) microscopy. Embryo recordings started ~20 minutes after fertilisation, while the female pronucleus is completing its meiotic divisions, until the 4 cell stage, ~30 minutes later.

10 In the F1 progeny of control worms that were either not injected, or injected with irrelevant dsRNA, the cellular events of the first two rounds of embryonic cell division were found to exhibit very limited variability, as observed by DIC microscopy. All processes that were examined and scored for the possibility of phenotypic deviations are listed and illustrated in Figure 1. Briefly, the antero-posterior polarity of the embryo is initially determined by the position of the male pronucleus at the cortex, shortly after entry into the egg (right arrow in Fig. 1a). This is accompanied by a clear, coordinated flow of yolk granules through the central portion of the cytoplasm along the embryo's longitudinal axis towards the male pronucleus, and a concomitant series of cortical waves or ruffles progressing towards the anterior of the embryo (left side in Fig.1). Shortly thereafter, the male and female pronuclei undergo highly patterned migrations (right and left arrows respectively, in Fig. 1a,b) resulting in their meeting within the posterior half of the embryo (Fig. 1c), followed by a centration and rotation (Fig. 1d) of the pronuclear pair and associated centrosomes (arrowheads in Fig. 1b-d) to set up the future mitotic spindle along the embryo's longitudinal axis. After synchronous breakdown of the pronuclear envelopes, the clearly bipolar mitotic spindle is initially short (Fig. 1e), but then elongates while exhibiting clear lateral "rocking" movements of the posterior pole (Fig. 1f-h). These movements are accompanied by a slight posterior displacement of the posterior spindle pole, while the anterior spindle pole remains approximately stationary. This then results in an asymmetric positioning of the spindle during anaphase and telophase, thereby yielding an asymmetric placement of the cytokinetic furrow (arrowheads in Fig. 1i,j), and generating unequally-sized daughter cells: a smaller posterior P1 blastomere (right cell in Fig. 1k-o), and larger anterior AB blastomere (left cell in Fig. 1k-n). While the AB nucleus

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then migrates directly to the center of the AB cell (left arrow in Fig. 1k-l), the P1 nucleus typically migrates further towards the posterior of that cell (right arrow in Fig. 1k-l), before undergoing a pronounced 90° rotation while re-migrating to the anterior P1 cortex with one of its duplicated centrosomes leading (arrowheads in Fig. 1m). This insures that the P1
5 blastomere then divides along the embryo's longitudinal axis, perpendicular to that of the AB blastomere (Fig. 1n, arrowheads indicate centrosomes). These two divisions occur asynchronously, with P1 lagging 2-3 minutes behind AB (Fig. 1 n-p).

In the F1 embryos of worms injected with dsRNAs "300C3" or "340G12", the following highly reproducible phenotypes are observed (Fig. 2). First, although the dynamics of
10 female pronuclear migration appear normal in all cases, its initiation is often somewhat delayed. Meeting and apposition of the two pronuclei also typically exhibits defects in that the female pronucleus gets captured by only one of the two centrosomes associated with the male pronucleus (compare Fig. 2a-c with Fig. 1a-c). Although this defect is usually corrected before pronuclear envelope breakdown is completed, subsequent positioning of
15 the mitotic spindle within the embryo often appears defective. Weak manifestation of this phenotype appears as a lack of rocking of the posterior spindle pole during anaphase, while more severe cases show a notable drift of the entire spindle towards the posterior or lateral cortex, reaching the cortex itself and losing its longitudinal alignment completely. In the latter cases, the strongly aberrant spindle position gives rise to inappropriate specification
20 of cleavage furrow formation, leading to anomalous cytokinesis. Even in cases where spindle position appears relatively normal, positioning of the daughter Nucleus-Centrosomes-Complexes (NCCs) typically appears abnormal as soon as anaphase ends and the cleavage furrow ingresses. This is often particularly visible in the AB blastomere, where the NCC, instead of moving directly to the centre of the cell starting at telophase,
25 first migrates anteriorly in close proximity to the lateral cortex before eventually centering (Fig. 2a-k). This defect is usually accompanied by an apparent absence of interzonal spindle microtubules at telophase and a notable bifurcation or forking of the cytokinetic cleavage furrow (arrows in Fig. 2 g), leading to aberrantly-sized daughter blastomeres or even failure of cytokinesis by complete regression of the furrow (Fig. 2g-m). Nuclear
30 migration and positioning of the P1 nucleus is also aberrant in most cases, resulting in a significant delay - or in some cases, a complete failure - in achieving its expected 90° rotation and association with the anterior cortex. Division of the P1 blastomere is often

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significantly delayed in such embryos. Finally, defects in female meiotic divisions are also occasionally observed, as evidenced by the presence of multiple female pronuclei, indicating a failure to successfully extrude one or both polar bodies, which could come from cytokinetic defects similar to those noted above.

5 All observed phenotypes indicate a requirement for H38K22.2 gene function in the microtubule-dependent cellular positioning of NCCs and spindles during mitosis, and possibly meiosis. Since this function is essential to cell cycle progression and cell division throughout metazoans, this gene and any homologues and derivatives thereof represent excellent tools for use in the development of a wide range of therapeutics including anti-
10 proliferative agents. Analysis of the H38K22.2 gene sequence reveals clear orthologues in human (NCBI Accession # AAH09478), mouse (NCBI Accession # AAF04863) and *Drosophila* (NCBI Accession # CG7427) (see Fig. 5), all of which have had no known functions ascribed to them until now. Based on their extremely high level of sequence conservation at the protein level, it can be concluded that all of these genes most likely
15 encode proteins with equivalent functions in each of their respective species. The 336 residue protein encoded by the H38K22.2 gene isoform "a" exhibits no known structural motifs or consensus domains, according to either SMART or CDD analyses.

20 **EXAMPLE 4: Characterization of the *C. elegans* gene C02F5.1**

A dsRNA, "307C1", was designed and used to specifically silence the expression of the *C. elegans* gene C02F5.1 by RNAi, thereby testing its functional involvement in the first 2 rounds of embryonic cell division in this metazoan species. The dsRNA was synthesized *in*
25 *vitro* from a PCR-amplified wild type genomic DNA fragment of the C02F5.1 gene. For the PCR, oligonucleotides with sequences "ATCTGAAGATCCGTCCACT" and "ATGCACAATGGGTATTTTT" were used as forward and reverse primers, respectively, to generate dsRNA "307C1" which was purified, and injected into adult hermaphrodite worms. The phenotypic consequences of the RNAi treatment were documented 24 hours
30 later in the F1 progeny of injected worms, using time-lapse differential interference contrast (DIC) microscopy. Embryo recordings started ~20 minutes after fertilisation,

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while the female pronucleus is completing its meiotic divisions, until the 4 cell stage, ~30 minutes later.

In the F1 progeny of control worms that were either not injected, or injected with irrelevant dsRNA, the cellular events of the first two rounds of embryonic cell division were found to exhibit very limited variability, as observed by DIC microscopy. All processes that were examined and scored for the possibility of phenotypic deviations are listed and illustrated in Figure 1.

F1 embryos from parent worms injected with dsRNA "307C1" are consistently found to exhibit the following phenotypes (Fig. 3). First, all cellular processes that are scorable by DIC microscopy until entry into mitosis are typically indistinguishable from the wild type pattern. These include egg shape and size, yolk granule size and density, yolk granule flows and cortical ruffling, pseudo-cleavage furrow formation and positioning, pronuclear appearance (arrows in Fig. 3a) and migration (Fig. 3a,b), as well as centration and rotation of pronuclei (Fig. 3b,c) and associated pair of centrosomes (arrowheads in Fig. 3b,c). Formation and positioning of the bipolar mitotic spindle also take place normally, but the spindle is most often thinner and less rigid than in wild type, exhibiting aberrant lateral bending during its rocking and elongation at anaphase (Fig. 3f-i). After completion of cytokinesis, which appears normal, the reforming daughter nuclei are typically tear-shaped, and remain close to the newly-formed cortex for a prolonged period (Fig. 3a and k). Consistent with the tear shape, the two nuclei remain often physically connected by anomalous chromatin bridges and karyomeres are also typically seen (asterisks in Fig. 3k and l). This phenotype subsequently results in embryonic lethality in all cases.

The absence of defects in pronuclear migration and assembly of the bipolar spindle argue against a role for this gene in more general microtubule functions. The observed defects are consistent with a failure in mitotic chromosome segregation, most likely in the separation of sister chromatids, resulting in the formation of chromatin bridges, which then persist at telophase. The present data therefore indicate an essential requirement for C02F5.1 gene function in mitotic chromosome segregation. Since this function is essential to cell cycle progression and cell division throughout metazoans, this gene and any

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homologues and derivatives thereof represent excellent tools for use in the development of a wide range of therapeutics including anti-proliferative agents.

Analysis of the C02F5.1 sequence reveals that the encoded 1010 residue protein contains regions predicted to form coiled coil structures, i.e. likely protein-protein interaction domains. Sequence homology analyses using the BLASTp program presently reveal no clearly orthologous sequences in other organisms. However, considering the essential and highly conserved nature of the cellular process in question, functional orthologues of this gene/protein are extremely likely to exist in all metazoans, possibly in all eukaryotes, and will be identified using for example the methodology as outlined in EXAMPLE 6.

10

EXAMPLE 5: Characterization of the *C. elegans* gene F10E9.8

15

Two dsRNAs, "305A12" and "341G5", were designed and used to specifically silence the expression of the *C. elegans* gene F10E9.8 by RNAi, thereby testing its functional involvement in the first 2 rounds of embryonic cell division in this metazoan species. The dsRNAs were synthesized *in vitro* from PCR-amplified wild type genomic DNA fragments of the F10E9.8 gene. For PCR, two sets of primer pairs were used: "TTCGTCTCGAACACGTATATCCT" with "GAAAGAAGATGAATCAGGCATTG" as forward and reverse primers, respectively, to generate dsRNA "305A12", and "CTGCAAAAATTATGACTGTGTCG" with "AGCATTGAGATTGTTGTCC" as forward and reverse primers, respectively, to generate dsRNA "341G5". The dsRNA was purified, and injected into adult hermaphrodite worms. The phenotypic consequences of the RNAi treatment were documented 24 hours later in the F1 progeny of injected worms, using time-lapse differential interference contrast (DIC) microscopy. Embryo recordings started ~20 minutes after fertilisation, while the female pronucleus is completing its meiotic divisions, until the 4 cell stage, ~30 minutes later.

In the F1 progeny of control worms that were either not injected, or injected with irrelevant dsRNA, the cellular events of the first two rounds of embryonic cell division were found to

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exhibit very limited variability, as observed by DIC microscopy. All processes that were examined and scored for the possibility of phenotypic deviations are listed and illustrated in Figure 1.

In the F1 embryos of worms injected with dsRNAs "305A12" or "341G5", the following
5 highly reproducible phenotypes are observed (Fig. 4). First, all cellular processes that are scorable by DIC microscopy until the 2-cell stage are typically indistinguishable from the wild type pattern. These include egg shape and size, yolk granule size and density, yolk granule flows and cortical ruffling, pseudo-cleavage furrow formation and positioning, pronuclear appearance (arrows in Fig. 4a) and migration (Fig. 4a,b), as well as centration
10 and rotation of pronuclei (Fig. 4b,c) and associated pair of centrosomes (arrowheads in Fig. 4b,c). The first round of division also occurs without any detectable deviations from wild type (Fig. 4d-h). It should particularly be noted that no defects are observed with respect to size, number or positioning of centrosomes or spindle poles in the single cell embryo (note arrowheads in Fig. 4b-f). In the two-cell stage embryo, however, although nuclear
15 positioning also remains equivalent to wild type, an apparent failure in centrosome duplication is consistently observed in one of the two blastomeres and sometimes in both. A single perinuclear centrosomal region, as seen by its exclusion of yolk granules (black arrowhead in Fig. 4h-j), is typically observed instead of the two normally seen both in wild type embryos and in the unaffected blastomere (white arrowheads in Fig. 4i,j). Despite the
20 apparent failure in centrosome duplication, microtubule-dependent processes continue normally, as illustrated by the successful anterior migration of the P1 nucleus, with its single centrosomal region leading (black arrowhead in Fig. 4h-j). Upon entering mitosis, as scored by nuclear envelope breakdown, the defective blastomere then fails to generate a bipolar spindle, forming instead a monopolar array of microtubules (dashed circle in Fig.
25 4k), as evidenced by the radial alignments of yolk granules in that region. Cytokinesis fails to occur in that blastomere, resulting in reformation of multiple, irregularly sized nuclei, known as karyomeres (arrows in Fig. 4m,n). In contrast, all aspects of cell division occur normally in the neighboring blastomere, resulting in normal daughter cells, each containing a single equal-sized nucleus (arrows in Fig. 4l).

30 The complete failure in bipolar spindle formation, accompanied by the presence of a single centrosomal region instead of two in the affected two-cell stage blastomere, clearly

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indicates a requirement for F10E9.8 gene function in the complex process of mitotic spindle assembly. However, the lack of detectable defects in other microtubule-dependent processes including pronuclear migration and spindle function in the single-cell embryo effectively rules out a general microtubule-related function. In view of the maternal nature
5 of the RNAi effect and the fact that the egg inherits its first centrosome paternally, the successful generation of a bipolar spindle in the single-cell embryo further suggests that F10E9.8 function may, in fact, be required for some aspect of centrosome duplication or separation.

Indeed, since sperm development is fully completed within the parent before initiation of
10 the RNAi treatment, it remains unaffected by the injected dsRNA. This results in the donation of an intact "wild type" centrosome from the sperm to the egg at fertilisation. After fertilisation, this already bipartite centrosome (i.e. containing two "replication units", as evidenced by the presence of two centrioles) undergoes one round of duplication, as
15 observed in other systems by the budding of a new centriole barrel from each existing centriole. This is followed by a physical separation of the two centriole pairs and associated pericentriolar material. This process is not dependent on the prior duplication event, and is solely needed to insure the successful formation of the bipolar spindle to be
used in the first round of embryonic cell division. It therefore appears that F10E9.8 function is most likely not required for this process.

20 5. If the first duplication round fails, however, bipolar spindle formation is expected to fail during the second round of division, as seen here. Interestingly, the fact that this failure often occurs only in one of the two blastomeres suggests that in these cases only one of the original centrosome's two "replication units" actually failed in its first round of duplication at the single-cell stage. This observation is consistent with findings from other eukaryotes
25 indicating that one of the two replication units contained within the sperm's centrosome actually comes into the egg already fully equipped for one duplication round, while the other must rely on cytoplasmic factors within the egg to permit its own duplication (Sluder, G., Hinchcliffe EH. Control of centrosome reproduction: the right number at the right time. *Biol. Cell.* 91, 413-27 (1999)).

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The present findings therefore suggest that the requirement for F10E9.8 function in mitotic spindle assembly most likely results from this gene's essential role in the process of centrosome duplication.

5 Since the process of spindle assembly is essential to cell cycle progression and cell division throughout metazoans, this gene and any homologues and derivatives thereof represent excellent tools for use in the development of a wide range of therapeutics including anti-proliferative agents. Analysis of the F10E9.8 sequence reveals that the encoded 1207
10 residue protein contains one large region predicted to form coiled coil structures, i.e. likely protein-protein interaction domains, and four predicted transmembrane domains. Sequence homology analyses using the BLASTp program presently reveal no clearly orthologous sequences in other organisms. However, considering the essential and highly conserved nature of the cellular process in question, functional orthologues of this gene/protein are extremely likely to exist in all metazoans, possibly all eukaryotes, and will be identified
15 using for example the following methodology.

EXAMPLE 6: Protocol for identifying functional orthologues in other species

20 The present invention describes genes identified as having essential functions in cell division in the model organism *C. elegans*. The basis for performing research in model organisms is that the newly discovered functions for the genes in *C. elegans* will be conserved in other species including humans. Cell division is highly conserved during evolution and therefore the approach of discovering a gene function in *C. elegans* and
25 using the information to characterise or assign functions for the human orthologue is well justified. There are two themes of conservation of genes during evolution. A gene sequence may be conserved. This means that the DNA nucleotide sequence of the gene is very similar in different species, which in turn suggests that the function of the gene is the same in the different species. As is known to any person skilled in the art, a sequence
30 identity or homology above a particular level defines that two genes in different species code for the same gene product and gene function. Homologous genes are typically

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identified by performing blast analysis with appropriate software, or by other approaches. For a blast search, an e-value of 10^{-30} will extract the significant homologous sequences. Further phylogenetic analysis can be performed to identify which of the extracted sequences are the orthologues.

- 5 Therefore the following example for identification of orthologues can be presented. A blast search is performed using the blast sequence analysis programs and an e-value of 10^{-3} . An alternative parameter can be the percentage of sequence identity. Over 100 residues, a sequence identity of 30% defines a homologous gene. After the blast search is completed, multiple sequence alignment is performed using appropriate software (for example,
10 CLUSTALW) and a neighbour joining phylogenetic tree is generated. Any person skilled in the art can identify the human orthologue from a phylogenetic tree. Essentially, the human sequence that is separated on the tree by a single speciation event or most closely related on the tree is likely to be an orthologue.

- The second theme of conservation is that the gene function can be conserved with greater
15 divergence of sequence. In the present invention this theme of conservation is not defined. However, if other genes are discovered to have functions that result in the gene product being identified as the same gene product as those claimed in the present invention then the present claims also apply to such genes.

Claims

1. An isolated nucleic acid molecule encoding a polypeptide functionally involved in cell division and proliferation or a fragment thereof and comprising a nucleic acid sequence selected from the group consisting of:
 - (a) the nucleic acid sequences presented in SEQ ID NO. 1 to 3, SEQ ID NO. 4 to 5, SEQ ID NO. 6 to 7, SEQ ID NO. 12 and fragments thereof and their complementary strands,
 - (b) nucleic acid sequences encoding polypeptides that exhibit a sequence identity with SEQ ID NO. 8, SEQ ID NO. 9, SEQ ID NO. 10, SEQ ID NO. 11 or SEQ ID NO. 13 of at least 25 % over 100 residues and/or which are detectable in a computer aided search using the blast sequence analysis programs with an e-value of at most 10^{-30} ,
 - (c) nucleic acid sequences which are capable of hybridizing with the nucleic acid sequences of (a) or (b) under conditions of medium/high stringency,
 - (d) nucleic acid sequences which are degenerate as a result of the genetic code to any of the sequences defined in (a), (b) or (c).
2. A nucleic acid probe comprising a nucleic acid sequence as defined in claim 1 which may be a polynucleotide or an oligonucleotide comprising at least 15 nucleotides containing a detectable label.
3. A recombinant vector or nucleic acid construct having incorporated therein the isolated nucleic acid molecule of claim 1 or a fragment thereof.
4. The vector of claim 3 which is an expression vector.
5. A host cell which has been genetically engineered to incorporate therein the isolated nucleic acid molecule of claim 1 or the recombinant vector or nucleic acid construct of claim 3.
6. The host cell of claim 5 having incorporated therein the expression vector of claim 4.

7. An assay kit comprising the isolated nucleic acid molecule or a fragment thereof of claim 1 or the probe of claim 2 in a suitable container.

5 8. A method for producing a polypeptide functionally involved in cell division and proliferation or a fragment thereof in a host cell comprising the steps

(a) transferring the expression vector of claim 4 into a suitable host cell, and

(b) cultivating the host cells of step (a) under conditions which will permit the expression of said polypeptide or fragment thereof and

10 (c) optionally, secretion of the expressed polypeptide into the culture medium.

9. Use of a probe as defined in claim 2 to isolate orthologues of genes comprising the nucleic acid sequences as disclosed in SEQ ID NO. 1 to 3, SEQ ID NO. 4 to 5, SEQ ID NO. 6 to 7, SEQ ID NO. 11.

15

10. Use of the isolated nucleic acid molecule or a fragment thereof as defined in claim 1 for producing a polypeptide functionally involved in cell division and proliferation or a fragment thereof.

20 11. Use of a nucleic acid molecule or a fragment thereof as defined in claim 1 or of the probe of claim 2 in a screening assay for interacting drugs that inhibit, stimulate or effect the cell division or proliferation.

25 12. Use of a nucleic acid molecule as defined in claim 1 or of the probe of claim 2 in a method for diagnosis or treatment of diseases associated with anomalous and/or excessive cell division or proliferation.

30 13. The use of claim 12 wherein the disease is a coronary restenosis or a neoplastic disease selected from the group consisting of lymphoma, lung cancer, colon cancer, ovarian cancer and breast cancer.

14. A polypeptide functionally involved in cell division and proliferation or a fragment thereof comprising an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequences depicted in SEQ ID NO. 8, 9, 10, 11 and 13 and fragments thereof,
- (b) amino acid sequences which exhibit a sequence identity with the sequences of (a) of at least 25 % over 100 residues and/or which are detectable in a computer aided search using the BLAST sequence analysis programs with an e-value of at most 10^{-30} ,
- (c) amino acid sequences encoded by any of the nucleic acid sequences (c) – (d) as defined in claim 1.
15. A fusion protein comprising the polypeptide or fragment thereof of claim 14.
16. An antibody or a fragment thereof capable of specifically binding with the polypeptide of claim 14 or with an immunogenic part thereof.
17. A humanized antibody capable of specifically binding with the polypeptide of claim 14 or with an immunogenic part thereof.
18. An assay kit comprising the polypeptide as claimed in claim 14, the fusion protein as claimed in claim 15, or the antibodies as claimed in claims 16 and/or 17 in a suitable container.
19. Use of the polypeptide of claim 14, of the fusion protein of claim 15, or of the antibodies of claims 16 or 17 in a screening assay for interacting drugs that inhibit, stimulate or effect the cell division or proliferation.
20. The use of a polypeptide or of an antibody as claimed in claim 19 wherein the screening assay for interacting drugs comprises the following steps:

1. recombinant expression of said polypeptide in a host cell
2. isolation and optionally purification of the recombinantly expressed polypeptide of step 1
3. optionally labelling of the drugs that are tested to interact with said polypeptide and/or labelling of the recombinantly expressed polypeptide
4. immobilization of the recombinantly expressed polypeptide to a solid phase
5. binding of a potential interaction partner or a variety thereof to the polypeptide
6. optionally one or more washing steps
7. detection and/or quantification of the interaction, in particular by monitoring the amount of label remaining associated with the solid phase over background levels.

21. Use of the polypeptide of claim 14, of an amino acid sequence as defined in claim 14 or of the antibodies of claims 16 or 17 in a method for diagnosis or treatment of diseases associated with anomalous and/or excessive cell division or proliferation.

22. The use of claim 20 wherein the disease is a coronary restenosis or a neoplastic disease selected from the group consisting of lymphoma, lung cancer, colon cancer, ovarian cancer and breast cancer.

22. Use of the nucleic acid sequences as defined in claim 1 or the amino acid sequences as defined in claim 14 for developing computational models, structural models or other models for evaluating drug binding and efficacy.



FIG. 1

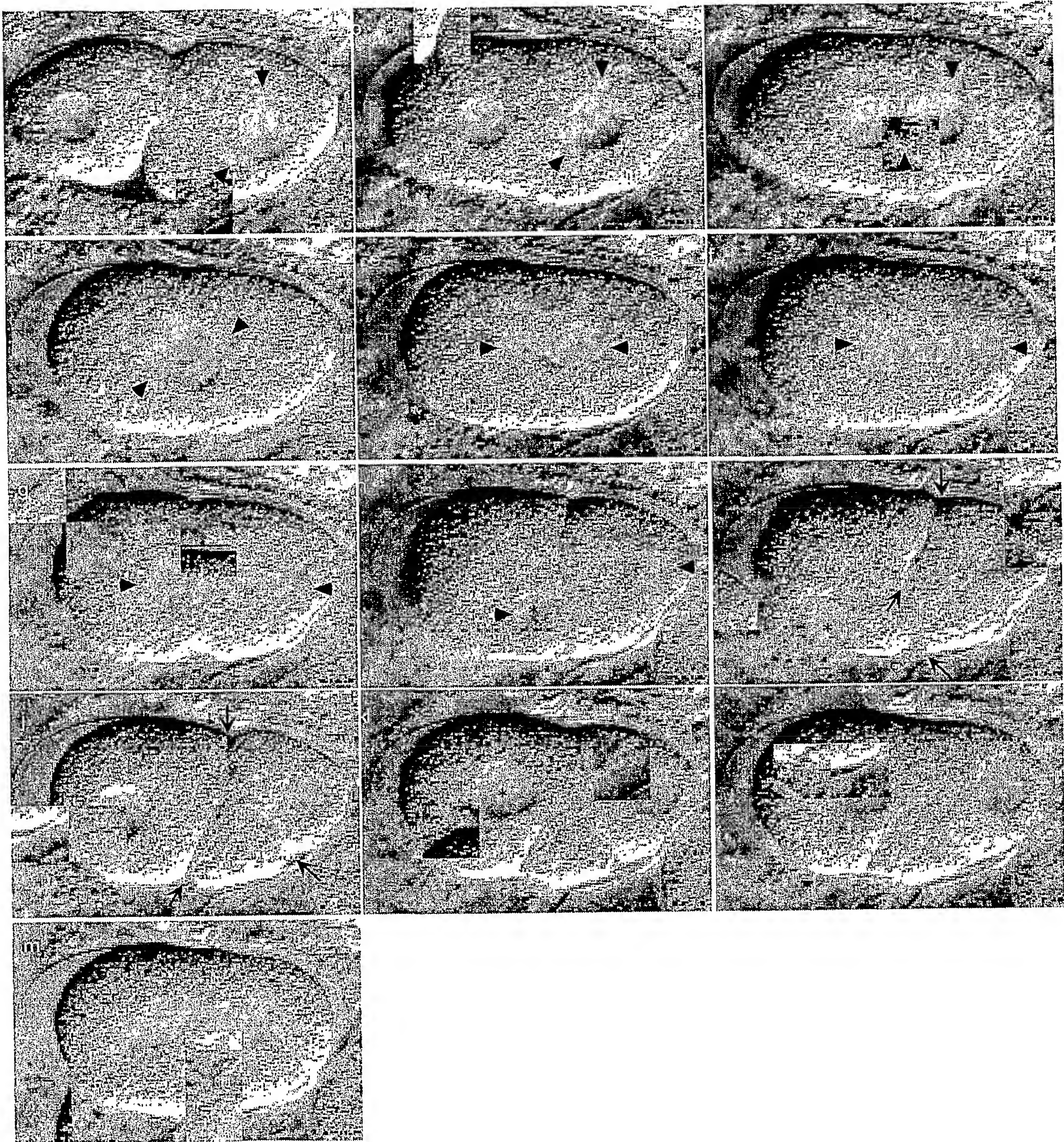


FIG. 2

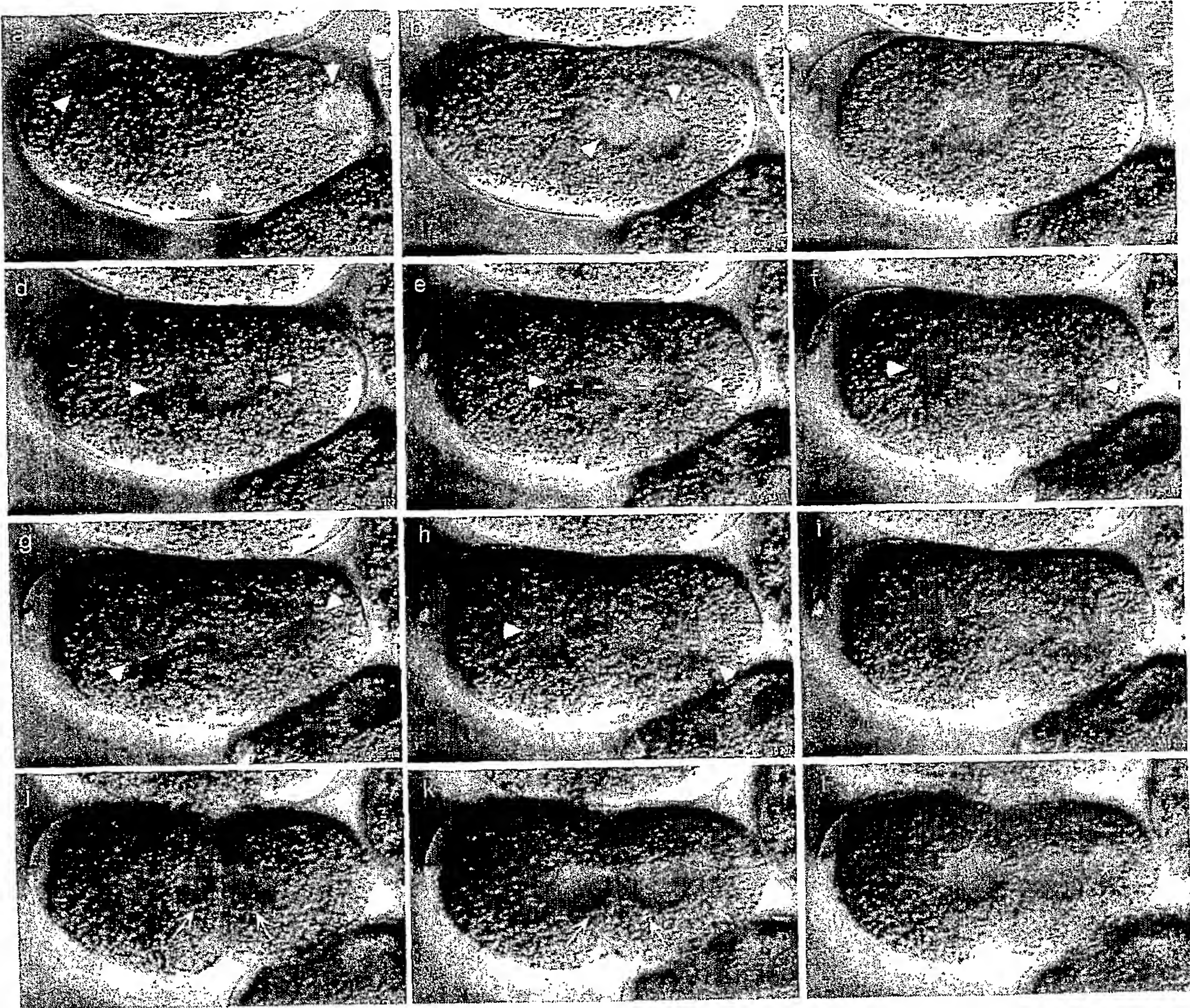


FIG. 3

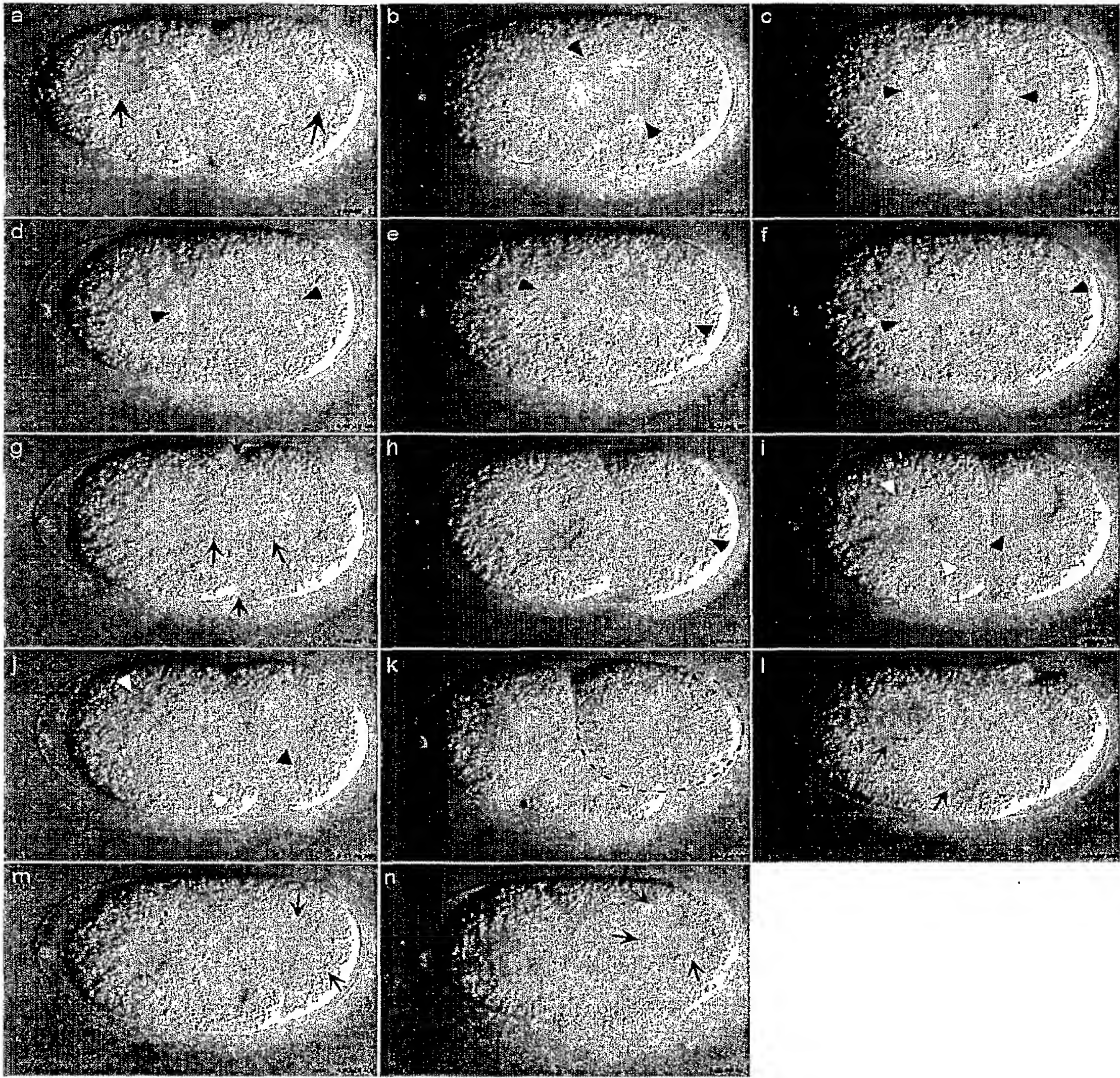


FIG. 4

Multiple Sequence Alignment of the H38K22.2a family

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CeH38K22.2b ---MNRLLKS-DQ-----
DmCG7427 MILONKLLKSSTHRDKVKKFISLTHTGQATATFCLOQNDWKFFELASDNYFONPEYYYRE--
MmAAF04863 ---MNRLLKS-SQDKVROEMI FTOSSEKTAVSCLSONDWKLDVATDNFFONPELYIRESV
HsAAH09478 ---MNRLLKS-SQDKVROEMI FTOSSEKTAVSCLSONDWKLDVATDNFFONPELYIRESV

CeH38K22.2a QPSVDRSNIERLFNQYVDEKDKVGEKRMGPHGINRLLTDLGYEATDRRVLVLAWKETAQT
CeH38K22.2b -----KTKTERLFNQYVDEKDKVGEKRMGPHGINRLLTDLGYEATDRRVLVLAWKETAQT
DmCG7427 ---LDRKRTEOLFMRYSRDESD---PLKIGSQGVHIFLEDLDLKPDSKLVLTAWKTHAEV
MmAAF04863 KGSIDRKKLEQHYTRYKDEQD---ENKIGIDGTQQFCDDIALDPASISVLTAWKERAAT
HsAAH09478 KGSIDRKKLEQLYNRYKDEQD---ENKIGIDGTQQFCDDIALDPASISVLTAWKERAAT

CeH38K22.2a QCEESLDEWVKGMTALQADTVQNLQRQIDSINSGLESQKAKFHELYLFAENYAKSAACRN
CeH38K22.2b QCEESLDEWVKGMTALQADTVQNLQRQIDSINSGLESQKAKFHELYLFAENYAKSAACRN
DmCG7427 QCEESRDEFINGMCDLIGDSIDKLTKEPILEQELN-DAGKFKDFYHETENYAKDPGQKG
MmAAF04863 QCEESKQEFMDGMTLGCDSIEKLKAQTPKMEQELK-EPGRFKDFYQETENFAKNPGQKG
HsAAH09478 QCEESKQEFMDGMTLGCDSIEKLKAQTPKMEQELK-EPGRFKDFYQETENFAKNPGQKG

CeH38K22.2a LDLETAICCWDLFGQSTIMTQWIDFLWAQENAAASRLAQNVGASNAKQFKSVWISRDT
CeH38K22.2b LDLETAICCWDLFGQSTIMTQWIDFLWAQENAAASRLAQNVGASNAKQFKSVWISRDT
DmCG7427 IDLEMAIAYWCVLSGRFKFLDIWCOFLEEKHKRAIS-----RDT
MmAAF04863 LDLEMAIAYWNLVLNGRKFFLDLWNKELLEHHKRSIP-----KDT
HsAAH09478 LDLEMAIAYWNLVLNGRKFFLDLWNKELLEHHKRSIP-----KDT

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CeH38K22.2b WNLFWDFEILLSKPDLSDYDDEGAWPVLIDQFVDYCRENLNYPKPGNASNDQQMETPKIAQ
DmCG7427 WNLILLDFATNIDDRMSNYDSEGAWPVLIDDFEVEWCQENDHLKEDSSPASGYQQQSSASS
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HsAAH09478 WNLILLDESTMIADDMSNYDEEGAWPVLIDDFEVEFARPQIAGTKSTTV-----

CeH38K22.2a KKPGIFYFNSNLQLIEFKLFQYPMLKTIFKITIHTAGTNR
CeH38K22.2b KKPGIFYFNSNLQLIEFKLFQYPMLKTIFKITIHTAGTNR
DmCG7427 SQKNISSAYQTSNSTNMNYG-----
MmAAF04863 -----
HsAAH09478 -----

Statistics	HsAAH09478	MmAAF04863	DmCG7427
CeH38K22.2a	E-value: 1e-49 Identities: 101/275 (36%) Positives: 158/275 (56%)	E-value: 7e-49 Identities: 100/275 (36%) Positives: 157/275 (56%)	E-value: 6e-44 Identities: 104/299 (36%) Positives: 154/299 (56%)
CeH38K22.2b	E-value: 1e-35 Identities: 78/214 (36%) Positives: 118/214 (54%)	E-value: 7e-35 Identities: 77/214 (35%) Positives: 117/214 (56%)	E-value: 2e-36 Identities: 86/238 (36%) Positives: 126/238 (52%)

FIG. 5

CE61773US.ST25
SEQUENCE LISTING

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<120> Eukaryotic cell division genes and their use in diagnosis and treatment of proliferative diseases

<130> CE61773US

<150> US 60/246,750

<151> 2000-11-09

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CE61773US.ST25

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Ile	Glu	Arg	Leu	Phe	Asn	Gln	Tyr	Val	Asp	Pro	Lys	Asp	Lys	Val	Gly
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Glu	Lys	Arg	Met	Gly	Pro	His	Gly	Ile	Asn	Arg	Leu	Leu	Thr	Asp	Leu
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Leu	Asp	Leu	Glu	Thr	Ala	Ile	Cys	Cys	Trp	Asp	Val	Leu	Phe	Gly	Gln
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Asn Ser Asn Leu Gln Leu Ile Glu Phe Lys Leu Phe Gln Tyr Pro Met
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Pro His Gly Ile Asn Arg Leu Leu Thr Asp Leu Gly Tyr Glu Ala Thr
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Asp Arg Arg Val Leu Val Leu Ala Trp Lys Phe Thr Ala Gln Thr Gln
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Cys Glu Phe Ser Leu Asp Glu Trp Val Lys Gly Met Thr Ala Leu Gln
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Ala Asp Thr Val Gln Asn Leu Arg Gln Arg Ile Asp Ser Ile Asn Ser
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Gly Leu Glu Ser Asp Lys Ala Lys Phe His Glu Leu Tyr Leu Phe Ala
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Phe Asn Tyr Ala Lys Ser Ala Ala Cys Arg Asn Leu Asp Leu Glu Thr
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Thr Gln Trp Ile Asp Phe Leu Trp Ala Gln Glu Asn Ala Ala Ala Ser
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Arg Leu Ala Gln Asn Val Gly Ala Ser Asn Ala Lys Gln Phe Lys Ser
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Val Trp Ile Ser Arg Asp Thr Trp Asn Leu Phe Trp Asp Phe Ile Leu
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Val Leu Ile Asp Gln Phe Val Asp Tyr Cys Arg Glu Asn Leu Asn Tyr
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Pro Lys Pro Gly Asn Ala Ser Asn Asp Gln Gln Met Glu Thr Pro Lys
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Ile Ala Gln Lys Lys Pro Gly Ile Phe Tyr Phe Asn Ser Asn Leu Gln
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Lys	Gln	Tyr	Asp	Arg	Asp	His	Gly	Lys	Ile	Leu	Asp	Ala	Thr	Pro	Val		
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		115					120					125					
Thr	Thr	Arg	Asp	Pro	Thr	Leu	Leu	Tyr	Glu	Lys	Ile	Val	Glu	Thr	Thr		
	130					135					140						
Thr	Lys	Val	Thr	Glu	Arg	Ile	Val	Ser	Met	Pro	Leu	Asp	Asp	Thr	Leu		
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Ala	Met	Phe	Asn	Thr	Thr	Asn	Gln	Glu	Asp	Lys	Asp	Met	Ser	Val	Asp		
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Ser 385	Thr	Lys	Tyr	Pro	Ser 390	Ile	Ala	Asp	Glu	Val 395	Glu	Asp	Leu	Asp	Met 400
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Pro Ala Arg Val Lys Ile Gly Ala Asn Asn Ser Ile Ile Asp Ser Gln
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Asp Gly Thr Leu Thr Leu Pro Lys Ser Asn Val Glu Val Thr Thr Thr
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Asn Asp Val Tyr Thr Ser Leu Glu Arg Gln Glu Glu Asn Ala Ser Glu
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Asn Val Ser Met Ile Asn Glu Ser Ser Val His Ser Glu Ile Asp Lys
 515 520 525

Lys Ser Phe Met Leu Ile Glu Glu Glu Arg Ala Phe Met His Ser Ser
 530 535 540

Met Ile Asp Val Ala Gln Lys Leu Glu Asp Asp Gly Ser Ser Lys Thr
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Pro Val Ile Leu Ala Ser Gln Ser Ala Ser Leu Ala Thr Lys Glu Pro
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Ser Ala Leu His Asn Ser Ser Ala Thr Leu Asn Asn Ser Met Glu Leu
 580 585 590

Asp Asn Asn Thr Leu Leu Lys Thr Met Gln Ile Thr Thr Cys Glu Asp
 595 600 605

Ile Ser Met Val His Glu Ser Ile Ala Val Glu Leu Asn Ser Asn Lys
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Glu Gln Glu Gln Phe Gly Asp Glu Thr Leu Gln Lys Asn Asp Thr Ser
 625 630 635 640

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Thr	Glu	Tyr	Arg	Gln	Asn	Lys	Thr	Met	Gln	Thr	Ser	Gln	Asp	Ser	Met
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Pro	Ser	Met	Ser	Leu	Asn	Asp	Ser	Gly	Arg	Asp	Ile	Leu	Ala	Met	Asn
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Asn Phe
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Ser	Ser	Pro	His	Leu	Ser	Ser	Phe	Phe	Asp	Ile	Gly	Cys	Gly	Phe	Leu	
		35					40					45				
Ser	Pro	Asn	Asn	Lys	Asn	Ala	Met	Asn	Thr	Ser	His	Asn	Ser	Phe	Phe	
	50					55					60					
Phe	Phe	Leu	Leu	Leu	Phe	Leu	Phe	Ser	Phe	Phe	Leu	Pro	Phe	Ala	Ile	
65					70					75					80	
Gln	Leu	Phe	Gly	Lys	Leu	Pro	Asn	Ser	Lys	Lys	Met	Trp	Ala	Phe	Pro	
				85					90					95		
Ala	Ile	Leu	Ser	Ile	Asn	Val	Asn	Leu	Ile	Ser	Arg	Lys	Leu	Met	Val	
			100					105					110			
Thr	Val	Ile	Pro	Lys	Ile	Ile	Ser	Ser	Pro	Tyr	Pro	Arg	Thr	Arg	Leu	
		115					120					125				
Pro	Leu	Tyr	Leu	Tyr	Thr	Val	Ser	Ile	Ile	Ile	Ser	Cys	Ser	Leu	Leu	
	130					135					140					
Tyr	Trp	Asn	Leu	Leu	Tyr	Cys	Lys	Asn	Tyr	Asp	Cys	Val	Val	Glu	Lys	
145					150					155					160	
Glu	Phe	Arg	Trp	Gly	Ser	Thr	Arg	His	Leu	Leu	Gln	Tyr	Phe	Pro	Val	
				165					170					175		
Ile	Ala	Ala	Pro	Ile	Ile	Met	Val	Ile	Ser	Phe	Ser	Trp	Leu	Ile	Ile	
			180					185					190			
Ala	Ile	Tyr	Tyr	Ser	Ser	Ser	Ser	Cys	Val	Leu	Thr	Phe	Asn	Phe	Met	
		195					200					205				
Glu	Met	Pro	Ser	Ala	Val	Leu	Cys	Ser	Leu	Leu	Gly	Gly	Ile	Ser	Ser	

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210

215

220

Val Ile Glu Ile His Phe Ser Ile Glu Val Asn Gln Val Gln Trp Thr
 225 230 235 240

Asp Gln Trp Leu Leu Ser Ser Val Gly Leu Pro Ile Asn Asp Cys Leu
 245 250 255

Lys Ile Asp Ile Phe Arg Asp Leu Gln Tyr Phe Tyr Ala Phe Tyr Met
 260 265 270

Leu Gln Leu Arg Ser His Phe Asn Asn Pro Ser Asn Ile Phe Glu Phe
 275 280 285

Pro Ile Phe Phe Lys Ser Met Asn Gln Lys Tyr Tyr Val Asn Cys Asp
 290 295 300

Ile Tyr Ser Cys Ser Ile His Phe Met Lys Lys Gln Lys Lys Met Ser
 305 310 315 320

Phe Ser Gln Ala Gln Asp Val Tyr Leu Arg Leu Lys Gln Glu Lys Glu
 325 330 335

Glu Glu Lys Gln Arg Glu Arg Ala Glu Arg Glu Lys Arg Asn Glu Thr
 340 345 350

Ile Ala Ala Thr Asn Lys Ser Arg Lys Lys Met Asn Gln Ala Leu Ala
 355 360 365

Lys Arg Asn Lys Lys Gly Gln Pro Asn Leu Asn Ala Gln Met Asp Met
 370 375 380

Ala Ser Asp Glu Asn Ile Gly Ala Asp Gly Glu Gln Lys Pro Ser Arg
 385 390 395 400

Pro Phe Leu Arg Lys Gly Gln Gly Thr Ala Arg Phe Arg Met Val Val
 405 410 415

Cys Ala Asn Thr Arg Leu Ile Glu Ile Ile Tyr Glu Val Gln Pro Arg

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420

425

430

Asn Asn Lys Thr Ser Ala Gly Ala Pro Pro Thr Ser Glu Leu Ser Ser
 435 440 445

Ala Ser Ser Pro Ser Ile Asn Val Pro Arg Phe Ser Leu Ser Asn Ala
 450 455 460

Leu Pro Asn Ser Ala Arg Thr Val Asp Ser Gly Ile Ser Asn Glu Asp
 465 470 475 480

Glu Thr Arg Pro Pro Thr Thr Ala Ser Leu Pro Met Asp Gln Pro Ser
 485 490 495

Leu Ser Ser Ser Pro Glu Asn Arg Leu Asn Pro Ala Pro Ser Val Ala
 500 505 510

Glu Glu His Gly His Ser Gly Gln His Ala Glu Glu Glu Glu Asp Asn
 515 520 525

Asp Thr Asp Glu Val Ser Ala Met Pro Ser Phe Val Pro Asp Glu Pro
 530 535 540

Ser Thr Leu Val Asn Ser Asp His Glu Leu Ser Asp Asp Ala Leu Lys
 545 550 555 560

Tyr Lys Asn Ala Ala Ala Glu Phe Lys Ala Phe Glu Arg Arg Met Asp
 565 570 575

Ser Met Arg Ser Ala Ser Thr Ile Thr Thr Ser Leu Ala Thr Pro Ser
 580 585 590

Ser Cys Ala Pro Ser Asn Ser Ser Glu Pro Pro Thr Arg Ser Thr Pro
 595 600 605

Ile Met Asn Asp Leu Gly Val Gly Pro Asn Asn His Asn Trp Pro Ser
 610 615 620

Ser Met Gln Glu Leu Ser Gly Ile Ser Leu Glu Thr Pro Gln Ala Arg

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625					630					635					640
Pro	Leu	Gly	Ser	Asn	Arg	Ile	Asn	Gln	Leu	Val	Arg	Ser	Glu	Ala	Gln
				645					650					655	
Thr	Gly	Ile	Ser	Leu	Leu	Gln	His	His	Glu	Arg	Pro	Thr	Val	Thr	Ala
			660					665					670		
Pro	Leu	Arg	Arg	Asn	Asp	Met	Met	Asn	Ser	Ser	Arg	Gln	Asn	Pro	Gln
		675					680					685			
Asn	Gly	Asn	Val	Gln	Asp	Glu	Asn	Arg	Pro	Glu	His	Val	Tyr	Asp	Gln
	690					695					700				
Pro	Ile	His	Val	Pro	Gly	Ser	Ser	Leu	Asp	Arg	Gln	Lys	Leu	Glu	Ile
705					710					715					720
Glu	Ile	Arg	Arg	His	Arg	Asn	Leu	Asn	Ile	Gln	Leu	Arg	Asp	Thr	Ile
				725					730					735	
Ala	His	Leu	Asp	Tyr	Ala	Glu	Glu	Ser	Val	His	Thr	Thr	Lys	Arg	Gln
			740					745					750		
Leu	Glu	Glu	Lys	Ile	Ser	Glu	Val	Asn	Asn	Phe	Lys	Lys	Glu	Leu	Ile
		755					760					765			
Glu	Glu	Phe	Lys	Lys	Cys	Lys	Lys	Gly	Val	Glu	Glu	Glu	Phe	Glu	Lys
	770					775					780				
Lys	Phe	Glu	Lys	Ile	Lys	Glu	Asp	Tyr	Asp	Glu	Leu	Tyr	Glu	Lys	Leu
785					790					795					800
Lys	Arg	Asp	Gln	Arg	Asp	Leu	Glu	Arg	Asp	Gln	Lys	Ile	Leu	Lys	Lys
				805					810					815	
Gly	Thr	Gly	Glu	Arg	Asn	Lys	Glu	Phe	Thr	Glu	Thr	Ile	Ala	Thr	Leu
			820					825					830		
Arg	Asp	Lys	Leu	Arg	Ala	Ser	Glu	Thr	Lys	Asn	Ala	Gln	Tyr	Arg	Gln

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835

840

845

Asp Ile Arg Val Arg Asp Glu Lys Leu Lys Lys Lys Asp Glu Glu Ile
 850 855 860

Glu Lys Leu Gln Lys Asp Gly Asn Arg Leu Lys Ser Thr Leu Gln Thr
 865 870 875 880

Leu Glu Lys Arg Val Lys Gln Leu Arg Thr Glu Lys Glu Arg Asp Asp
 885 890 895

Lys Glu Lys Glu Met Phe Ala Lys Val Ala Met Asn Arg Lys Thr Ser
 900 905 910

Asn Pro Val Pro Pro Val Leu Asn Gln Ser Val Pro Ile Ser Ile Thr
 915 920 925

Ser Asn Gly Pro Ser Arg His Pro Ser Ser Ser Ser Leu Thr Thr Phe
 930 935 940

Arg Lys Pro Ser Thr Ser Asn Arg Glu Arg Gly Val Ser Trp Ala Asp
 945 950 955 960

Glu Pro Asn Glu Gln Ser Leu Glu Ala Val Pro Gln Glu Phe Leu Met
 965 970 975

Met Pro Val Lys Glu Met Pro Gly Lys Phe Gly Lys Cys Thr Ile Tyr
 980 985 990

Arg Asp Ser Leu Gly Glu Thr Ser Lys Val Thr Asp Thr Ile Ala Asn
 995 1000 1005

Gly Leu Leu Phe Glu Tyr Ser Asn Gly Asp Leu Arg Trp Val Asn
 1010 1015 1020

Arg Gln Asn Ala Val Asn Ile Tyr Ile Ser Ala Val Asp Lys Thr
 1025 1030 1035

Val Arg Ile Asp Leu Pro Thr Tyr Asn Ile Ser Ile Ile His Thr

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1040

1045

1050

Phe Gln Arg Gln Val Glu Val Leu Arg Pro Gly Asn Asn Ile Thr
 1055 1060 1065

Leu Ile Ser Ile Lys Arg Arg Glu Val Arg Thr Asp Leu Ile Tyr
 1070 1075 1080

Gln Asn Gly Met Tyr Lys Thr Glu Ile Phe Asn Arg Asp Gly Arg
 1085 1090 1095

Tyr Val Thr Lys Asp Phe Ser Asn Gln Glu Val Ser Arg Lys Tyr
 1100 1105 1110

Asn Pro Gly Thr His Thr Tyr Arg Asp Asn Gln Cys Arg Tyr Val
 1115 1120 1125

Leu Val Thr Asp Tyr Asn Asp Phe Glu Leu Val Glu Pro Glu Phe
 1130 1135 1140

Arg Leu Arg Trp Tyr Gln Gly Asp Pro Thr Gly Leu Asn Asn Gln
 1145 1150 1155

Tyr Ile Leu Lys Ile Ile Gly Arg Pro Glu Cys Ser Glu Lys Thr
 1160 1165 1170

Leu Arg Leu Glu Val Asn Leu Ser Thr Cys Glu Gly Thr Leu Glu
 1175 1180 1185

Thr Ala Glu Met Ile Gly Asp Lys Arg Arg Lys Thr Thr Leu Phe
 1190 1195 1200

Gln Trp Lys Lys
 1205

<210> 12
 <211> 780
 <212> DNA
 <213> homo sapiens

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<400> 12
atgaacaagt tgaaatcatc gcagaaggat aaagttcgtc agtttatgat cttcacacaa 60
tctagtga aaacagcagt aagttgtctt tctcaaaatg actggaagtt agatggttgc 120
acagataatt ttttccaaaa tcctgaactt tatatacgag agagtgtaaa aggatcattg 180
gacaggaaga agttagaaca gctgtacaat agatacaaag accctcaaga tgagaataaaa 240
attggaatag atggcataca gcagttctgt gatgacctgg cactcgatcc agccagcatt 300
agtgtgttga ttattgctgt gaagttcaga gcagcaacac agtgcgagtt ctccaaacag 360
gagttcatgg atggcatgac agaattagga tgtgacagca tagaacaact aaaggcccag 420
atacccaaga tggaacaaga attgaaagaa ccaggacgat ttaaggattt ttaccagttt 480
actttttaatt ttgcaaagaa tccaggacaa aaaggattag atctagaaat ggccattgcc 540
tactggaact tagtgcttaa tggaagattt aaattcttag acttatggaa taaatttttg 600
ttggaacatc ataaacgatc aataccaaaa gacacttgga atcttctttt agacttcagt 660
acgatgattg cagatgacat gtctaattat gatgaagaag gagcatggcc tgttcttatt 720
gatgactttg tggaatttgc acgccctcaa attgctggga caaaaagtac aacagtgtag 780

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<210> 13
<211> 259
<212> PRT
<213> homo sapiens

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<400> 13

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Met Asn Lys Leu Lys Ser Ser Gln Lys Asp Lys Val Arg Gln Phe Met
1          5          10          15

```

```

Ile Phe Thr Gln Ser Ser Glu Lys Thr Ala Val Ser Cys Leu Ser Gln
          20          25          30

```

```

Asn Asp Trp Lys Leu Asp Val Ala Thr Asp Asn Phe Phe Gln Asn Pro
          35          40          45

```

```

Glu Leu Tyr Ile Arg Glu Ser Val Lys Gly Ser Leu Asp Arg Lys Lys
          50          55          60

```

```

Leu Glu Gln Leu Tyr Asn Arg Tyr Lys Asp Pro Gln Asp Glu Asn Lys

```

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65

70

75

80

Ile Gly Ile Asp Gly Ile Gln Gln Phe Cys Asp Asp Leu Ala Leu Asp
85 90 95

Pro Ala Ser Ile Ser Val Leu Ile Ile Ala Trp Lys Phe Arg Ala Ala
100 105 110

Thr Gln Cys Glu Phe Ser Lys Gln Glu Phe Met Asp Gly Met Thr Glu
115 120 125

Leu Gly Cys Asp Ser Ile Glu Gln Leu Lys Ala Gln Ile Pro Lys Met
130 135 140

Glu Gln Glu Leu Lys Glu Pro Gly Arg Phe Lys Asp Phe Tyr Gln Phe
145 150 155 160

Thr Phe Asn Phe Ala Lys Asn Pro Gly Gln Lys Gly Leu Asp Leu Glu
165 170 175

Met Ala Ile Ala Tyr Trp Asn Leu Val Leu Asn Gly Arg Phe Lys Phe
180 185 190

Leu Asp Leu Trp Asn Lys Phe Leu Leu Glu His His Lys Arg Ser Ile
195 200 205

Pro Lys Asp Thr Trp Asn Leu Leu Leu Asp Phe Ser Thr Met Ile Ala
210 215 220

Asp Asp Met Ser Asn Tyr Asp Glu Glu Gly Ala Trp Pro Val Leu Ile
225 230 235 240

Asp Asp Phe Val Glu Phe Ala Arg Pro Gln Ile Ala Gly Thr Lys Ser
245 250 255

Thr Thr Val

<210> 14

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<211> 258
 <212> PRT
 <213> Homo sapiens

<400> 14

Ser Lys Gln Glu Phe Met Asp Gly Met Thr Glu Leu Gly Cys Asp Ser
 1 5 10 15

Ile Glu Gln Leu Lys Ala Gln Ile Pro Lys Met Glu Gln Glu Leu Lys
 20 25 30

Glu Pro Gly Arg Phe Lys Asp Phe Tyr Gln Phe Thr Phe Asn Phe Ala
 35 40 45

Lys Asn Pro Gly Gln Lys Gly Leu Asp Leu Glu Asp Arg Lys Lys Leu
 50 55 60

Glu Gln Leu Tyr Asn Arg Tyr Lys Asp Pro Gln Asp Glu Asn Lys Ile
 65 70 75 80

Gly Ile Asp Gly Ile Gln Gln Phe Cys Asp Asp Leu Ala Leu Asp Pro
 85 90 95

Ala Ser Ile Ser Val Leu Ile Ile Ala Trp Lys Phe Arg Ala Ala Thr
 100 105 110

Gln Cys Glu Phe Ser Lys Gln Glu Phe Met Asp Gly Met Thr Glu Leu
 115 120 125

Gly Cys Asp Ser Ile Glu Gln Leu Lys Ala Gln Ile Pro Lys Met Glu
 130 135 140

Gln Glu Leu Lys Glu Pro Gly Arg Phe Lys Asp Phe Tyr Gln Phe Thr
 145 150 155 160

Phe Asn Phe Ala Lys Asn Pro Gly Gln Lys Gly Leu Asp Leu Glu Met
 165 170 175

Ala Ile Ala Tyr Trp Asn Leu Val Leu Asn Gly Arg Phe Lys Phe Leu
 180 185 190

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Asp Leu Trp Asn Lys Phe Leu Leu Glu His His Lys Arg Ser Ile Pro
 195 200 205

Lys Asp Thr Trp Asn Leu Leu Leu Asp Phe Ser Thr Met Ile Ala Asp
 210 215 220

Asp Met Ser Asn Tyr Asp Glu Glu Gly Ala Trp Pro Val Leu Ile Asp
 225 230 235 240

Asp Phe Val Glu Phe Ala Arg Pro Gln Ile Ala Gly Thr Lys Ser Thr
 245 250 255

Thr Val

<210> 15
 <211> 19
 <212> DNA
 <213> artificial sequence

<220>
 <223> T7 polymerase promoter sequence (example 1)

<400> 15
 taatacgact cactatagg

19

<210> 16
 <211> 19
 <212> DNA
 <213> artificial sequence

<220>
 <223> T3 polymerase promoter sequence

<400> 16
 aattaaccct cactaaagg

19

<210> 17
 <211> 19
 <212> DNA
 <213> artificial sequence

<220>

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<223> oligonucleotide for PCR amplification (example 3)

<400> 17

tcaatcagta tgtcgaccc

19

<210> 18

<211> 19

<212> DNA

<213> artificial sequence

<220>

<223> oligonucleotide for PCR amplification (example 3)

<400> 18

ggaagaaatt ggggaaaca

19

<210> 19

<211> 19

<212> DNA

<213> artificial sequence

<220>

<223> oligonucleotide for PCR amplification (example 3)

<400> 19

atcgagcgcc tcttcaatc

19

<210> 20

<211> 19

<212> DNA

<213> artificial sequence

<220>

<223> oligonucleotide for PCR amplification (example 3)

<400> 20

tggtgtctcc atttgctga

19

<210> 21

<211> 19

<212> DNA

<213> artificial sequence

<220>

<223> oligonucleotide for PCR amplification (example 4)

<400> 21

atctgaagat ccgtccact

19

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<210> 22
<211> 19
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide for PCR amplification (example 4)

<400> 22
atgcacaatg ggtatTTTTT 19

<210> 23
<211> 23
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide for PCR amplification (example 5; forward
primer to generate dsRNA 305A12)

<400> 23
ttcgtctcga acacgtatat cct 23

<210> 24
<211> 23
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide for PCR amplification (example 5; reverse
primer to generate dsRNA 305A12)

<400> 24
gaaagaagat gaatcaggca ttg 23

<210> 25
<211> 23
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide for PCR amplification (example 5; forward
primer to generate dsRNA 341G5)

<400> 25
ctgcaaaaat tatgactgtg tcg 23

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<210> 26
<211> 21
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide for PCR amplification (example 5; reverse
primer to generate dsRNA 341G5)

<400> 26
agcattcaga tttggttgtc c

21